ALLELE	STANDARD	SEQUENCE	SEQ ID NO:	BINDIN
	PEPTIDE			AFFINITY
				(nM)
A*0101	944.02	YLEPAIAKY	3475	25
A*0201	941.01	FLPSDYFPSV	3476	5.0
A*0202	941.01	FLPSDYFPSV	3476	4.3
A*0203	941.01	FLPSDYFPSV	3476	10
A*0206	941.01	FLPSDYFPSV	3476	3.7
A*0207	941.01	FLPSDYFPSV	3476	23
A*6802	1141.02	FTQAGYPAL	3477	40
A*0301	941.12	KVFPYALINK	3478	11
A*1101	940.06	AVDLYHFLK	3479	6.0
A*3101	941.12	KVFPYALINK	3478	18
A*3301	1083.02	STLPETYVVRR	3480	29
A*6801	941.12	KVFPYALINK	3479	8.0
A*2402	979.02	AYIDNYNKF	3481	12
B*0702	1075.23	APRTLVYLL	3482	5.5
B*3501	1021.05	FPFKYAAAF	3483	7.2
B51	1021.05	FPFKYAAAF	3483	5.5
B*5301	1021.05	FPFKYAAAF	3483	9.3
B*5401	1021.05	FPFKYAAAF	3483	10

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le V. HLA Class II Standard Peptide Binding Affinity.

					12
Allele	Nomenclature	Standard	Sequence	SEQ ID	Bigging
		Peptide		NO:	Affinity
					(nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	3484	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	3485	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	3484	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	3486	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	3486	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	3487 ,	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	3487	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	3487	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	3487	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	3487	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	3488	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	3489	3.5
DRB1*1501	DR2w2β1	507.02	GRTQDENPVVHFFKNI	3490	9.1
			VTPRTPPP		
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	3491	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	3486	58
DRB5*0101	DR2w2β2	553.01	QYIKANSKFIGITE	3487	20
		1	<u> </u>		.l

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX. SF 1094066 v1

Conservancy	Freq.	Protein	Position	Sequence	SEQ ID NO:	String	A*0101
95	19	POL	521	AICSVVRRAF	1 ,	XIXXXXXXX	
95	19	NUC	54	ALRQAILCW	2	XLXXXXXX	
80	16	₽₩	108	AMOWNSTTF	3	XMXXXXXXF	
100	20	POL	166	ASFCGSPY	4 . 5	XSXXXXXY XSXXXXXXXW	
100 90	20 18	POL NUC	166 19	ASFCGSPYSW ASKLCLGW	6	XSXXXXXVV	
85	17	NUC	19	ASKLCLGWLW	7	xsxxxxxxx	
80	16	POL.	822	ASPLHVAW	8	xsxxxxx	
100 100	20 20	BW BW	312 312	CIPIPSSW	9 10	XIXXXXXW XIXXXXXXXF	
95	19	BW BW	253	CIPIPSSWAF CLIFLLVLLDY	11	XLXXXXXXXXX	
95	19	BW	239	CLRRFIIF	12	XLXXXXXF	
75	15	BW	239	CLRRFIIFLF	13	XLXXXXXXXF	
. 95 100	19 20	POL ENV	523 310	CSVVRRAF	1.4 1.5	XSXXXXXF XTXXXXXXXXW	
90	18	NUC	31	CTCIPIPSSW DIDPYKEF	16	XIXXXXXF	
85	17	NUC	29	DLLDTASALY	17	XLXXXXXXXY	11.1000
95 95	19	BW.	196 43	DSWWTSLNF	18 19	XSXXXXXXF XLXXXXXXXF	•
95	19 19	NUC .	43	ELLSFLPSDF ELLSFLPSDFF	20	XLXXXXXXXXF	
95	19	POL.	374	ESRLVVDF	21	XSXXXXXF	
95	19	POL	374	ESPLVVDFSQF	22	XSXXXXXXXF	
80 80	16 16	₽W	248 246	FILLLCLIF	23 24	XIXXXXXXXF	
95	19	BW BW	256	FLFILLLCLIF FLLVLLDY	25	XLXXXXXY	
95	19	POL	658	FSPTYKAF	26	XSXXXXXF	
90	18	. X	63	FSSAGPCALRF	27	XSXXXXXXXF	
100 95	20 19	EW POL	333 656	FSWLSLLVPF FTFSPTYKAF	28 29	XSXXXXXXXF	
95	19	. POL BW	346	FVGLSPTVW	30	XVXXXXXXX	
95	19	POL	627	GLLGFAAPF	31	XLXXXXXXF	
95 85	19	POL	509	GLSPFLLAQF	32	XLXXXXXXXF XMXXXXXXXF	
95	17 19	NUC NUC	29 123	GMDIDPYKEF GVWIRTPPAY	33 34	XVXXXXXXXX	0.0017
75	15	POL	569	HLNPNKTKRW	35	XLXXXXXXXW	
80	16	POL	491	. HLYSHPIILGF	36	XLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	
85 95	17 19	POL NUC	715 52	HTAELLAACF	37 38	XTXXXXXXXF XTXXXXXXXXW	
100	20	POL	149	HTALRQAILCW HTLWKAGILY	39	XTXXXXXXXX	0.0300
100	20	₽₩	249	ILLLCLIF	40	XLXXXXXF	
80	16	POL	760	ILRGTSFVY	41	XLXXXXXXY	0.0017
90 90	18 18	EW POL	188 625	ILTIPOSLDSW IVGLLGFAAPF	42 43	XLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	
80	16	POL	503	KIPMGVGLSPF	44	XIXXXXXXXXF	
85	17	NUC	21	KLCLGWLW	45	XLXXXXXW	
75 75	15 15	POL POL	108 108	KLIMPARF	46 47	XLXXXXXF XLXXXXXXY	0.0017
80	16	POL	610	KLIMPARFY KLPVNRPIDW	48	XLXXXXXXXW	
85	17	POL	574	KTKRWGYSLNF	49	XTXXXXXXXXF	
95	19	POL	55	KVGNFTGLY	50	XVXXXXXXY	0.0680 0.0084
95 100	19 20	EW POL	254 109	LIFLLVLLDY LIMPARFY	5 1 5 2	XIXXXXXXY XIXXXXXY	0.0004
85	17	NUC	30	LLDTASALY `	53	XLXXXXXXY	25.0000
80	16	POL	752	LLGCAANW	5 4	XDXXXXX	
95 100	19 20	POL EW	628 378	LLGFAAPF	55 56 ·	XLXXXXXF XLXXXXXXW	
100	20	BW	378	LLPIFFCLW	57	XLXXXXXXXXX .	•
95	19	NUC	44	LLSFLPSDF	58	XLXXXXXXF	
95	19	NUC	44	LLSFLPSDFF	59	XLXXXXXXXF	
90 95	18 19	POL EW	407 175	LLSSNLSW LLVLQAGF	60 61	XLXXXXXW XLXXXXXF	
95	19	₽W	175	LLVLQAGFF	62	XLXXXXXXF	
100	20	₽₩	338	LLVPFVQW	63	XDXXXXXW	
100 85	20	₽W	338	LLVPFVQWF	64 65	XLXXXXXXF XLXXXXXXXXF	
95	17 19	NUC NUC	100 45	LLWFHISCLTF LSFLPSDF	66	XSXXXXXF	
95	19	NUC	45	LSFLPSDFF	67	XSXXXXXXF	
95	19	POL	415	LSLDVSAAF	68	XSXXXXXF	4 2000
95 100	19 20	POL EW	415 336	LSLDVSAAFY	69 70	XSXXXXXXXXY XSXXXXXXXXW	4.2000
100	20	BW BW	336	LSLLVPFVQW LSLLVPFVQWF	71	XSXXXXXXXX	
95	19	×	53	LSLRGLPVCAF	72	XSXXXXXXXF	
95	19	POL	510	LSPFLLAGE	73	XSXXXXXF	
75 85	15 17	EW POL	349 742	LSPTVWLSVIW LSRKYTSF	74 75	XSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	
85	17	POL POL	742	LSRKYTSFPW	76	XSXXXXXXXW	
75	15	₽₩	16	LSVPNPLGF	. 77	XSXXXXXXF	
75	15	NUC	137	LTFGRETVLEY	78 ·	XTXXXXXXXXY	
90 90	18 18	BW BW	189 189	LTIPOSLDSW LTIPOSLDSWW	79 80	XTXXXXXXXW XTXXXXXXXXW	
90	18	POL.	404	LTNLLSSNLSW	81	XTXXXXXXXXW	
95	19	, BW	176	LVLQAGFF	82	XVXXXXXF	
100 100	20 20	EW POL	339	LVPFVQWF	83 84	XVXXXXXF XVXXXXXF	
85	17	BW	377 360	LVVDFSQF MMWYWGPSLY	85	XWXXXXXXXX	0.0810
75	15	x	103	MSTTDLEAY	86	XSXXXXXY	0.8500
75	15	×	103	MSTTDLEAYF	87	XSXXXXXXXF	

Conservancy	Freq.	Protein	Position	Sequence	SEQ ID NO:	String	A*0101
95	19	POL.	42	NLGNLNVSIPW	88	XLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	
90	18	POL.	406	NLLSSNLSW	89	XLXXXXXXXX	
95	19	POL.	45	NLNVSIPW	90	XFXXXXXXM	
75	15	BW	15	NLSVPNPLGF	9 1	XLXXXXXXXF	
90	18	POL	738	NSVVLSRKY	92	XSXXXXXXY	0.0005
100	20	BW	380	PIFFCLWVY	93	XIXXXXXXXY	0.0078
100	20	BW	314	PIPSSWAF	94	XIXXXXXF	
100	20	POL	124	PLDKGIKPY	95	XDXXXXXX	0.0190
100	20	POL	124	PLDKGIKPYY	96	XLXXXXXXXXY	0.1600
100	20	B/V	377	PLLPIFFCLW	97	XLXXXXXXXW	
95	19	B/V	174	PLLVLQAGF	98	XLXXXXXXF	
95	19	B/V	174	PLLVLQAGFF	99	XLXXXXXXXF	
80	16	POL	505	PMGVGLSPF	100	XMXXXXXXF	0.7700
. 85	17	POL	797	PTTGRTSLY	101	XTXXXXXXY	0.7700
75	15	BW.	351	PTVWLSVIW	102	xTxxxxxxxw	
85	17	POL	612	PVNRPIDW	103	XVXXXXXX	
95	19	POL	685	QVFADATPTG	104	xvxxxxxxxxw	
90	18	POL	624	RIVGLLGF	105	XIXXXXXF	
75	15	POL	106	RLKLIMPARF	106	XLXXXXXXXF	
75	15	POL	106	RLKLIMPARFY	107	XLXXXXXXXXY .	
95	19	POL	376	RLWDFSQF	108	XLXXXXXXF	
90 100	18	POL .	353	RTPARVTGGVF	109	XTXXXXXXXXF XIXXXXXXXXXF	
95	20	POL	49	SIPWTHKVGNF	110	XLXXXXXXXX	
95	19	ENV POL	194	SLDSWWTSLNF	111 112	XLXXXXXF	
95	19 19	POL	416 416	SLDVSAAF	113	XLXXXXXXY	17.2000
100	20	BW	337	SLDVSAAFY	114	XLXXXXXXW	17.2000
100	20	EW/	337	SLLVPFVQWF	115	XLXXXXXXXF	•
95	19	X	54	SLRGLPVCAF	116	XLXXXXXXXF	
90	18	â	64	SSAGPCALRF	117	XSXXXXXXXF	
75	15	x	104	STTDLEAY	118	XTXXXXXY	
75	15	x	104	STTDLEAYF	119	XTXXXXXXF	
75	15	EW.	17	SVPNPLGF	120	XVXXXXXF	
90	18	POL	739	SVVLSRKY	121	XVXXXXXXY	
85	17	POL	739	SVVLSRKYTSF	122	XVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	
90	18	BNV	190	TIPOSLDSW	123	XIXXXXXXXX	
90	18	₽₩	190	TIPQSLDSWW	124	XIXXXXXXXXW	
100	20	POL	150	TLWKAGILY	125	XLXXXXXXXY	0.0017
75	15	x	105 ·	TTDLEAYF	126	XTXXXXXF	
85	17	POL	798	TTGRTSLY	127	XTXXXXXY	
80	16	NUC	16	TVQASKLCLGW	128	XVXXXXXXXXXX	
75	15	BW.	352	TVWLSVIW	129	XVXXXXXX	
8.5	17	POL	741	VLSRKYTSF	130	XLXXXXXXF	
85	17	POL	741	VLSRKYTSFPW	131	XD00000000	
8.5	17	POL	740	VVLSRKYTSF	132	XVXXXXXXXXF	
80	16	. POL	759	WILAGTSF	133	XIXXXXXF	1
80	16	POL	759	WILRGTSFVY	134	XIXXXXXXXY	0.0023
95	19	NUC	125	WIRTPPAY	135	XIXXXXXY	
80	16	POL	751	WLLGCAANW	136	XLXXXXXXX	
95	19	POL	414	WLSLDVSAAF	137	XLXXXXXXXF	
95	19	POL.	414	WLSLDVSAAFY	138	XLXXXXXXXXX	
100	20	BW.	335	WLSLLVPF	139	XLXXXXXF	
100	20	BW BW	335	WLSLLVPFVQW	140	XLXXXXXXXXW	0.0810
85 95	17	NUC ON	26	WLWGMDIDPY	141	XLXXXXXXXY	0.0010
95 85	. 19	EW EW	237	WMCLRRFIIF	142	XMXXXXXXF	
100	17	BW ∞	359	WMMWYWGPS	143	XMXXXXXXXXY XTXXXXXF	
100	20	POL POL	52	WTHKVGNF	144	XLXXXXXXXXXY	
90	20 18	NUC NUC	122 118	YLPLDKGIKPY	145 146	XLXXXXXXX	
80	16	POL	493	YLVSFGVW	147	XSXXXXXXF	
85	17	POL	580	YSHPIILGF	147	XSXXXXXY	
0.5	17	ru	280	YSLNFMGY	148	A3AAAA1	

	5 A*6802								0.0470																																	
-	A.0206								0.2500																																	
	A.0203								3.3000																																	
ation)	A*0202				,				0.0340																																	
ng inform	A.0201					0.0001		٠	0.5000		0.0013							0.0001			0.0001			0.0010		0.0008			0.0093	0.0002	0.000	0.0004		0.0001								
(With bindi	AA.	11	. co	o	=	6	80	6	თ	80	O	10	-	œ	တ	10	80	o	Ξ	10	10	Ξ	œ	ග :	= :	<u></u>	Ξ,	æ (٥٢ و	0 0	no	· =	. 60	6	6	10	œ	=	œ	10	Ξ,	,
SUPER MOTIF (With binding information	SEQ ID NO:	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	1/2	173	1/4	173	17.0	178	179	180	181	182	183	184	185	186	187	188	50 00	25.
HBV A02 S	Sequence	AACEABSBSGA	AAMPHLLV	AANWILAGT	AAPFTGCGYPA	AICSVVRRA	AILCWGEL	AILCWGELM	ALMPLYACI	AMOWNSTT	AMSTTDLEA	AQFTSAICSV	AQFTSAICSVV	ATPTGWGL	ATPTGWGLA	ATPTGWGLAI	AVPNLQSL	AVPNLOSLT	AVPNLOSLTNL	CAANWILRGT	CAFSSAGPCA	CAFSSAGPCAL	CALRFTSA	CIPIPSSWA	CIPIPSSWAFA	CLAFSYMDDV	CLAFSYMDDVV	CLGWLWGM	CLGWLWGMDI	CLIFTAL		CLRRFIIFE	CLTFGRET	CLTFGRETY	COLDPARDV	COLDPARDVL	CORIVGIL	CORIVGLÍGFA	CQVFADAT	COVFADATPT	CICIPIPSSWA	727
	Position	721	431	756	632	521	28	58	642	108	102	516	516	069	069	069	397	397	397	755	61	61	69	312	312	533	533	5 6	23	253	030	239	107	107	7	7	622	622	684	684	310	7 X
	Protein	S	절	점	젙	절	3	3	젍	}	×	ರ	젍	젍	젍	점	절	젍	전	절	×	×	×	≥ i	≥ 6	<u>ප්</u> 8	ᅻ :	3 5	3 2	<u>}</u>	3 2	<u></u>	3	3	×	×	젙	절	점	점 :	≩ 8	ī
=	Frequency	17	17	16	19	19	18	18	19	16		19	19	19	16	15	19	19	19	16	19	6	&	50	9 :	∞ :	æ !	<u>~</u> :	\ - -	30	0 5	. 5	18	18	16	16	17	17	19	19	20	7
Table VIII	Conservancy	85	8 2	80	95	92	06	06	92	80	7.5	95	95	92	80	75	95	92	. 56	80	95	95	06	100	80	06	0.6	ກ ເ ໝໍ	8 .	2 5	و در	7.5	06	06	80	80	85	85	95	95	00 L	ŗ

Table VIII	≡			HBV A02 S	SUPER MOTIF (With binding information)	(With bindi	ng informa	tion)		*	
servancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	АА	A.0201	A.0202	A.0203	A.0206	A.6802
80	16	점	689	DATPTGWGLA	191	10					
7.5	15	절	689	DATPTGWGLAI	192	: =					
06	18	3	31	DIDPYKEFGA	193	10					
85	17	NC C	29	DLLDTASA	194	æ					
82	17	3	59	DLLDTASAL	195	6	0.0001				
95	19	헏	40	DUNIGNILNV	196	6	0.0004				
95	19	젍	40	DLNLGNLNVSI	197	Ξ					
80	16	2	32	DTASALYREA	198	10					
80	16	3	32	DTASALYREAL	199	Ξ					
92	19	×	14	DVLCLRPV	200	&					
92	19	×	14	DVLCLRPVGA	201	10	0.0001				
06	18	젇	541	DVVLGAKSV	202	6	0.0003				
100	20	헏	17	EAGPLEEL	203	6	0.0001				
80	16	×	122	ELGEEIP.	204	æ					
90	18	젅	718	ELLAACFA	205	œ					
7.5	15	3	142	ETVLEYLV	206	80					
92	19	절	687	FADATPTGWGL	207	Ξ					
85	17	전	724	FARSRSGA	208	80					
80	16	점	821	FASPLHVA	509	89					
92	19	젍	396	FAVPNLOSL	210	6					
92	19	절	396	FAVPNLOSLT	211	10	0.0003				
80	16	2	243	FIIFLFIL	212	89	0.0006				
80	16	2	243	FIIFLFILL	213	6	0.0002				
80	16	8	243	FIIFLFILL	214	10	0.0012				
80	16	8	248	FILLCLI	215	œ	0.0003				
80	16	8	248	FILLCLIF	216	10	0.0280				
80	16	8	248	FILLCLIFL	217	Ξ	0.0010				
80	16	≧	246	FLFILLCL	218	6	0.0002				
80	16	&	246	FLFILLCLI	219	10	0.0013				
7.5	15	2	171	FLGPLLVL	220	80					
7.5	15	2	171	FLGPLLVLOA	221	0	0.0190				
95	19	헏	513	FLLAQFTSA	222	6	0.2400				
92	19	점	513	FLLAQFTSAI	223	10	0.2100	0.0320	7.0000	0.1100	0.0880
. 95	19	젗	562	FLLSLGIHL,	224	თ	0.6500	0.0010	0.0100	0.1100	0.0035
80	16	2	183	FLLTRILT	225	œ					
80	16	8	183	FLLTRILTI	226	6	0.5100	0.0430	8.0000	0.2000	0.0010
95	19	8	256	FLIVILDYQGM	227	Ξ			٠		
100	20	점	363	FLVDKNPHNT	228	10	0.0012				
92	19	젍	929	FTFSPTYKA	229	6	0.0056	0.0150	0.0031	0.8000	7.3000
92	19	젗	. 959	FTFSPTYKAFL	230	=					
92	19	전	59	FTGLYSST	231	æ					
06	18	젍	29	FTGLYSSTV	232	6	0.0005				

A.6802																								0.0005																	
A*0206																								0.2800																	
A*0203																								0.0350																	
A*0202																								0.0003																	
A.0201		0.000	0.0024		0.0000	-	0.0008	0.0030						0.0001							0.0024		0.0049	0.4000	0.0008			0.0036	0.2800	0.0036						0.0002		0.0030		0.0031	
AA	80	o	10	œ	6	æ	10	10	Ξ	80	Ξ	80	=	6		œ	=	6	80	6	6	10	10	o.	0	80	Ξ	œ	-0	Ξ,	ω (æ ;	2 5	2 =	. œ	ာတ	10	 6	Ξ	6	
SEQ ID NO:	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	+07 190	202 966	267	268	269	270	271	272	273	
Sequence	FTQCGYPA	FTOCGYPAL	FTQCGYPALM	FTSAICSV	FTSAICSVV	FVGLSPTV	PVGLSPTVWL	PALGGCRHKL.	PALGGCRHKLV	FVQWFVGL	PVQWFVGLSPT	FVYVPSAL	FVYVPSALNPA	GAHLSLRGL	GAHLSLRGLPV	GAKSVQHL	GAKSVOHLESL	GIHLNPNKT	GILYKRET	GILYKRETT	GLCQVFADA	GLCQVFADAT	GLLGFAAPFT	GLLGWSPQA	GLPVCAFSSA	GLSPFLLA	GLSPFLLAQFT	GLSPTVWL	GLSPTVWLSV	GLSPTVWLSVI	GMLPVCPL	GIUNSVVL	GINESVENEL GTCE/W/PCA	GTSFVVPSAI	GVGISPE	GVGLSPFL	GVGLSPFLLA	GVWIRTPPA	HISCLTFGRET	HLVGSSGL	
Position	635	635	635	518	518	346	346	132	132	342	342	992	992	20	20	545	545	267	155	155	682	682	627	62	22	209	209	348	348	348	265	ςς ,	763	763	507	507	207	123	104	435	
Protein	젍	ಕ	ಶ	전	ರ್	8	}	×	×	}	}	전	전	×	×	전	전	전	전	절	젙	점	절	}	×	전	젍	2	≥	≥ :	₹	₫ 8	<u> </u>	2 2	2	<u>ද</u>	점	3	3	절	:
Frequency	19	19	19	19	19	19	19	18	18	19	19	18	18	19	18	17	17	15	18	18	17	17	19	17	19	19	19	20	15	15	80 9	10 L	. .	2 4	9 1	16	16	19	18	16	
Conservancy	95	95	9.5	95	95	95	92	06	06	92	92	06	06	92	06	85	85	7.5	06	06	85	85	92	82	95	92	92	100	7.5	75	06	1 0	c (2 6	0 80	80	80	95	06	80	

	A.6802			0.0530															0.0015						0.0067									0.0015)								
	A.0206			0.1700															0.1300						0.3100									0.5900									
	. A*0203	ł.		0.9300															0.0002						0.0770									2.7000									
(ion)	A.0202		. •	0.0003															0.0001						0.0085									0.0340									
g informat	A-0201			0.2200				0.0001		0.0001	0.0004	0.0002	0.0002				0.0002	0.0015	0.0190	0.0056		0.0160		0.0001	0.0210					0.0009			0.0001	0.0690					0.0001	0.0003	0.0001		
(With bindin	АА	=	80	6	&	=	80	6	8	o	æ	6	=	æ	10	80	o	6	10	=	80	10	89	6	0	=	æ	ω	œ ·	o (> -	<u> </u>	. 0	တ	10	=	æ	o	o	o	40	80	
SUPER MOTIF (With binding information)	SEQ ID NO:	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	305	306	307	308	309	310	311	312	313	314	315	316	
HBV A02 S	Sequence	HISLRGLPVCA	HLYSHPII	HLYSHPIIL	HTAELLAA	HTAELLAACFA	HTALROAI	HTALROAIL	HTLWKAGI	HTLWKAGIL	IIFIL	IIFLFILLL	IIFLFILLCL	IILGFRKI	IILGFRKIPM	ILCWGELM	ILGFRKIPM	ILLICLIFI	ILLCLIFIL	ILLICUFILV	ILRGTSFV	ILRGTSFVYV	ILSTLPET	ILSTLPETT	ILSTLPETTV	ILSTLPETTW	ILTIPOSL	LYKRETT	IVGLLGFA	WGLLGFAA	KAGII YKBETT	KIPMGVGI	KLCLGWLWGM	KLHLYSHPL	KLHLYSHPII	KLHLYSHPIIL	KLPVNRPI	KOAFTFSPT	KTKRWGYSL	KVCQRIVGL	KVCORIVGLL	KVGNFTGL	4
	Position	52	491	491	715	715	52	52	149	149	244	244	244	497	497	59	498	249	249	249	760	760	139	139	139	139	188	156	625	625	153	50.5	21	489	489	489	610	653	574	. 029	620	22	
	Protein	×	점	젍	절	절	3	3	전	젙	}	3	&	절	젙	3	전	8	8	₹	젗	절	3	3	3	3	}	ත් (전 :	덛 2	2 2	2	3	젒	점	정	점	점	전	전	정	ದ	
_	Frequency Protein	18	16	16	17	17	20	19	20	50	16	16	16	16	16	18	16	20	20	20	16	16	50	50	20	50	19	-	∞ :	- -	0 ¤	- -	17	19	16	16	16	19	19	17	17	19	
Table VIII	Conservancy	06	80	80	85	85	100	95	100	100	80	80	80	80	80	06	80	100	100	100	80	80	100	100	100	100	ဝ	06	06	06	0 6	0 0	8 2	95	80	80	80	95	92	85	85	95	

Table VIII				HBV A02 SU	SUPER MOTIF (With binding information)	(With bindir	ng informa	tion)			
Conservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	АА	A*0201	A.0202	. A*0203	A*0206	A.6802
85	17	×	91	KVLHKRTL	317	æ					
85	17	×	91	KVLHKRTLGL	318	10	0.0004				
06	18	ಶ	534	LAFSYMDDV	319	o	0.0002				
06	18	점	534	LAFSYMDDVV	320	10	0.0003				
90	18	ರ್ಷ	534	LAFSYMDDVVL	321	=					
95	- 6	ರ್ಷ	515	LAOFTSAI	322	æ					
92	1	점	515	LAOFTSAICSV	323	-					
100	50	2	254	LIFLLVLL	324	8	0.0025				
95	6	젍	514	LLAOFTSA	325	80					
95	19	전	514	LLAQFTSAI	326	6	0.1000	0.2700	3.7000	0.2600	0.7900
100	20	8	251	LICLIFIL	327	80	0.0004				
100	20	8	251	LICUFILV	328	6	0.0048				
100	20	≥	251	LICLIFILVL	329	10	0.0075				
100	20	<u>~</u>	251	LLCLIFILVIL	330	Ξ	0.0013				
85	17	3	30	LLDTASAL	331	∞					
98	19	8	260	LLDYGGML	. 332	80	0.0004				
90	18	8	260	LLDYOGMLPV	333	10	0.0980	0.0001	0.0200	0.6700	0.0009
80	16	점	752	LLGCAANWI	334	o	0.0011				
80	16	점	752	LLGCAANWIL	335	10	0.0140				
95	19	점	628	LLGFAAPFT	336	ō	0.0008				
85	17	2	63	LLGWSPQA	337	œ					
7.5	15	2	63	LLGWSPQAQGI	338	11					
100	20	2	250	LLLCLIFL	339	89	9000.0				
100	20	2	250	LLLCLIFIL	340	o	0.0065				
100	20	2	250	LLICUFLLV	341	10	0.0036				
100	50	<u>~</u>	250	LLICUFLLYL	342	=	0.0005				
100	20	8	378	LLPIFFCL	343	89	0.0055				
100	50	<u>~</u>	378	LLPIFFCLWV	344	10	0.0320	0.0008	0.0150	0.8000	0.0005
92	6	젗	263	LLSLGIML	345	80					
06	18	젇	407	LLSSNLSWL	346	o.	0.0110	0.0780	3.9000	0.2700	0.0100
06	8	절 :	407	LLSSNLSWLSL	347	=					
80	16	2	184	LLTRILTI	348	œ	0.0026				
80	16	ದ್ದ	436	LLVGSSGL	349	80					
92	19	2	257	гглгтрходм	350	10	0.0050				
95	19	8	257	LLVLLDYGGML	351	Ξ					
06	18	2	175	LLVLQAGFFL	352	10	0.0310	0.0037	0.0045	0.1500	0.0110
06	18	8	175	LLVLOAGFFLL	353	=	0.0074				
95	19	8	338	LLVPFVQWFV	354	10	0.6700	0.3800	1.7000	0.2900	0.1400
06	18	2	100	LLWFHISCL	355	თ	0.0130	0.0002	0.0420	0.3100	0.0098
82	17	3	100	LLWFHISCLT	356	0					
92	19	젍	643	LMPLYACI	357	æ					
95	19	8	178	LOAGFFL	358	80					
				_							

Table VIII	=			HBV A02 SI	V A02 SUPER MOTIF (With binding information)	(With bindi	ng informa	tion)			
nservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	AA	A-0201	A-0202	A-0203	A.0206	A.6802
95	19	8	178	LOAGFFLLT	359	o					
80	16	8	178	LOAGFFLLTRI	360	Ξ					
100	20	점	401	LOSLTNLL	361	80					
95	19	3	108	LTFGRETV	362	œ					
7.5	15	3	137	LTFGRETVL	363	6					
06	18	점	404	LTNLLSSNL	364	6					
80	16	2	185	LTRILTIPOSL	365						
85	17	점	66	LTVNEKRAL	366	G					
100	50	점	364	LVDKNPHNT	367	6	0.0001				
98	19	8	258	LVLLDYOGM	368	6	0.0001				
98	19	8	258	LVLLDYQGML	369	10	0.0001				
06	18	8	176	LVLOAGFFL	370	6	9600.0				
06	18	8	176	LVLOAGFFLL	371	10	0.0022				
90	18	8	176	LVLQAGFFLLT	372	Ξ					
95	19	8	339	LVPFVQWFV	373	6	0.0420	0.0150	0.0048	0.7900	2.8000
95	19	8	339	LVPFVQWFVGL	374	-					
90	18	3	119	LVSFGVWI	375	80	0.0004				
06	18	3	119	LVSFGVWIRT	376	10					
85	17	8	360	MMWYWGPSL	37.7	6	0.6400				
7.5	15	2	-	MOLFHLCL	378	æ					
100	20	3	136	NAPILSTL	379	æ					
100	20	3	136	NAPILSTLPET	380	=					
92	19	점	42	NLGNLNVSI	381	6	0.0047				
06	18	절	406	NITSSNISWL	382	10	0.0016				
98	19	젍	45	NLNVSIPWT	383	6	0.0005				
100	20	젍	400	NLOSLTNL	384	œ					
100	20	절	400	NLOSLTNLL	385	თ	0.0047				
75	15	8	15	NLSVPNPL	386	80					
06	18	ğ	411	NLSWLSLDV	387	თ	0.0650	0.0051	0.6400	0.1600	0.0990
06	18	점	411	NLSWLSLDVSA	388	Ξ					
100	20	전	47	NVSIPWTHKV	389	10	0.0001				
100	20	헏	430	PAAMPHLL	390	œ					
85	17	정	430	PAAMPHLLV	391	თ					
06	18	정	775	PADDPSRGRL	392	10					
06	18	8	131	PAGGSSSĞT	393	თ				٠	
90	18	2	131	PAGGSSSGTV	394	10					
92	19	점	641	PALMPLYA	395	80					
92	19	젗	641	PALMPLYACI	396	0	0.0001				
75	15	×	145	PAPCNFFT	397	œ					
75	5	×	145	PAPCNFFTSA	398	10					
08 ¦	9 :	× ;	= :	PARDVLCL P1997 01 P21	555	ω ,					
0	<u>.</u>	<	=	PAROVICIARV	20	=					

Table VIII	=			HBV A02 S	SUPER MOTIF (With binding information	(With bindi	informa	tion)		٠	
nservancy	Frequency Protein	Protein	Position	Sequence	SEQ ID NO:	AA	A-0201	A.0202	A*0203	A.0206	A.6802
06	18	8	355	PABVTGGV	401	α					
	8	2	35.5	PARVTGGVE	402	, C					
06	18	වූ	355	PARVTGGVFLV	403	-					
95	19	3	130	PAYRPPNA	404	. 60					
95	19	S S	130	PAYRPPNAPI	405	10	0.0001				
95	19	3	130	PAYRPPNAPIL	406	=					
85	17	점	616	PIDWKVCQRI	407	10	0.0001				
85	17	젙	616	PIDWKVCQRIV	408	=					
100	20	2	380	PIFFCLWV	409	æ	-				
100	50	2	380	PIFFCLWYI	410	10	0.0004				
85	17	젒	713	PIHTAELL	411	æ					
85	17	점	713	PIHTAELLA	412	o					
85	17	젗	713	PIHTAELLAA	413	10					
80	16	정	496	PIILGFRKI	414	6	0.0001				
80	16	전	496	PIILGFRKIPM	415	Ξ					
100	20	3	138	PILSTLPET	416	6	0.0001				
100	20	3	138	PILSTLPETT	417	10	0.0001				
100	20	3	138	PILSTLPETTV	418	=	0.0001				
80	16	2	314	PIPSSWAFA	419	6					
95	19	젍	20	PLEEELPRL	420	б	0.0003				
90	18		20	PLEEELPRLA	421	10	0.0001				
92	19	2	10	PLGFFPDHOL.	422	10	0.0005				
100	20	점	427	PLHPAAMPHL	423	10	0.0001				
00	20	젒	427	PLHPAAMPHLL	424	=					
100	20	26	377	PLLPIFFCL	425	6	0.0650	0.0001	0.0018	0.1100	0.0047
100	20	≥	377	PLLPIFFCLWV	426	=					
06	18	8	174	PLLVLQAGFFL	427	=	0.0008				
80	16	젙	711	PLPIHTAEL	428	თ	0.0004				
80	16	젍	711	PLPIHTAELL	429	10	0.0001				
80	16	젇	711	PLPIHTAELLA	430	Ξ					
75	15	젇	2	PLSYOHFRKL	431	10	0.0001				
75	15		2	PLSYOHFRKIL	432	Ξ					
85	17	젍	86	PLTVNEKRRL	433	01	0.0001				
80	16	젍	202	· PMGVGLSPFL	434	01	0.0001				
80	16	점	505	PMGVGLSPFLL	435	Ξ				٠	
95	19	<u>8</u>	106	POAMOWNST	436	6					
80	16	8	106	POAMOWNSTT	437	10					
06	18	8	192	POSLDSWWT	438	6					
06	18	2	192	POSLDSWWTSL	439	Ξ					
75	15	ಶ	692	PTGWGLAI	440	60					
80	16	8	219	PTSNHSPT	441	89					
82	17	ೱ	797	PTTGRTSL	442	80					

AA A 70201 A 70202 A 70203 A 70206 8 10 8 10 8 11 1	Table VIII	=			NDV AUZ S	AUZ SUPER MOTH (With binding Information	(with bindir	ig informa	llon		
17 POL 797 PTTGRTSLYA 444 444 6 6 6 6 6 6 6	Sonservancy	Frequency	Protein	Position	Sequence	NO:	AA	A.0201	A.0202	. A*0203	A.0206 A.6802
16	85	17	ğ	797	PTTGRTSLYA	443	10				
16 NLC 15 PTVQASSIGLCL 445 10 15 BW 351 PTVWLSNIM 447 10 15 RW 351 PTVWLSNIM 447 10 17 POL 654 QAFTESPTYKA 448 8 10 19 POL 654 QAFTESPTYKA 450 8 11 19 POL 654 QAFTESPTYKA 450 8 11 10 BW 179 QAGFELTRI 452 8 11 11 BW 179 QAGFELTRI 453 10 12 BW 179 QAGFELTRI 455 10 13 RNC 57 QALLOWGEM 456 11 14 RNC 57 QALLOWGEM 456 10 15 RW 107 QAMOWINST 465 9 16 X 8 QLIDPABION 460 8 16 X 8 QLIDPABION 460 8 16 X 8 QLIDPABION 465 9 16 X 8 QLIDPABION 465 9 17 RNC 99 QLILWFHISCL 465 9 18 RNC 58 QALLOWGEM 477 11 19 POL 528 RAFPICLA 466 9 10 RNC 58 RAFPICLA 466 9 11 RNC 58 RAFPICLA 466 9 12 RNC 58 RAFPICLA 466 9 13 RNC 58 RAFPICLA 466 9 14 RNC 58 RAFPICLA 466 9 15 RNC 58 RALLOWGEL 477 11 16 RNC 58 RALLOWGEL 477 11 17 RW 88 ROSCROPT 478 8 18 RNC 35 RAPEDIUL 478 8 19 POL 35 RAPEDIUL 481 8 10 RNC 36 RAPEDIUL 481 8 11 RNC 36 RAPEDIUL 481 8 12 POL 31 RAPERSPILAN 481 8 13 RNFASSIL 481 8 14 RNFASSIL 481 8 15 POL 31 RNFASSIL 481 8 16 POL 31 RNFASSIL 481 8 17 RNF RASPIL 481 8 18 RNF RASPIL 481 8 19 POL 357 RNFGSNET 481 8 10 RNC 381 RNFRASPIL 481 8 11 RNFRASPIL 481 8 12 POL 357 RNFGSNET 481 8 13 RNFRASPIL 481 8 14 RNFRASPIL 481 8 15 POL 357 RNFGSNET 481 8 15 POL 357 RNFGSNET 481 8 16 RNFRASPIL 481 8 17 RNFRASPIL 481 8 18 RNFRASPIL 481 8 19 RNFRASPIL 481 8 10 RNFRASPIL 481 8 11 RNFRASPIL 481 8 11 RNFRASPIL 481 8 12 RNFRASPIL 481 8 13 RNFRASPIL 481	80	16	3	15	PTVQASKL	444	80			•	
15 BW 351 PTWMLSVI 446 8 8 15 K 351 PTWMLSVI 447 10 10 10 10 10 10 10 1	80	16	3	15	PTVQASKLCL	445	10				
15 BW 351 PTVMLSVWMM 447 10 19	7.5	15	8	351	PTVWLSVI	446	œ				
19 X 59 PVCAESSA 448 8 19 POL 642 OAFTESPTYKA 449 10 19 POL 654 OAFTESPTYKA 451 11 19 POL 654 OAFTESPTYKA 451 11 16 BW 179 OAGFALITRIL 452 8 16 BW 179 OAGFALITRIL 452 10 16 BW 179 OAGFALITRIL 452 11 18 NLC 57 OALLCWGELM 455 9 19 BW 107 OAMCWNISTT 456 10 16 X 8 QLDPARDAL 466 9 16 X 8 QLDPARDAL 466 <t< td=""><td>7.5</td><td>15</td><td>2</td><td>351</td><td>PTVWLSVIWM</td><td>447</td><td>10</td><td></td><td></td><td></td><td></td></t<>	7.5	15	2	351	PTVWLSVIWM	447	10				
17 POL 612 PNNFPIDWWV 449 10 19 POL 654 OAFTESPT 450 8 19 POL 654 OAFTESPT 451 11 16 BW 179 OAGFTLITI 452 8 16 BW 179 OAGFTLITI 453 10 18 NUC 57 OAULOWGELM 455 11 19 BW 179 OAGFTLITI 456 11 19 BW 107 OAMOWNST 455 10 10 BW 107 OAMOWNST 455 10 10 RW 107 OAWICWGELM 456 10 10 K 8 OLDPARDV 462 11 11 NUC 18 OASKLCIGW 462 11 10 K 8 OLDPARDV 465 10 11 NUC 99 OLUWFHISCL 465 10 10 POL 624 RIVIELICA 466 8 11 POL 624 RIVIELICA 466 10 18 POL 624 RIVIELICA 466 10 19 POL 624 RIVIELICA 466 10 10 RUC 624 RIVIELICA 466 10 11 RUC 56 ROALICWGEL 477 11 11 BW 88 ROLLWPHISCL 477 11 11 BW 88 ROLLWPHISCL 478 8 12 POL 106 RIVIELINA 477 11 13 POL 56 ROALICWGEL 477 11 14 POL 58 ROALICWGEL 477 11 15 POL 58 ROALICWGEL 478 8 16 POL 58 ROALICWGEL 478 8 17 BW 88 ROESGROPT 478 8 18 POL 58 ROALICWGEL 480 8 19 POL 58 ROALICWGEL 480 8 10 POL 58 ROALICWGEL 480 8 11 POL 58 ROALICWGEL 480 8 12 POL 58 ROALICWGEL 480 8 13 RVHFASPL 481 8 14 POL 58 RVHFASPL 481 8 15 POL 58 RVHFASPL 481 8 16 POL 58 RVHFASPL 481 8 17 POL 58 RVHFASPL 481 8 18 POL 58 RVHFASPL 481 8 19 POL 58 RVHFASPL 481 8 10 POL 58 RVHFASPL 481 8 10 POL 58 RVHFASPL 481 8 11 POL 58 RVHFASPL 481 8 11	95	19	×	29	PVCAFSSA	448	80				
19 P.CL 654 OAFTESPT 450 8 19 P.CL 654 OAFTESPTYKA 451 11 10 P.CL 654 OAFTESPTYKA 451 11 11 NLC 57 OAGGFELTRI 452 10 12 NLC 57 OAGGFELTRI 455 10 13 NLC 57 OAGGFELTRI 456 10 14 NLC 57 OAGGFELTRI 456 10 15 P.CL 18 OASIGCLOWL 456 10 16 X 8 OLDAADVL 460 8 16 X 8 OLDAADVL 461 11 16 X 8 OLDAADVL 461 11 17 NLC 99 OLLWFHISCL 463 10 18 NLC 99 OLLWFHISCL 465 10 19 P.CL 624 RAPPLCA 466 8 10 P.CL 624 RAPPLCA 466 10 11 P.CL 624 RAVICLORA 466 10 12 P.CL 624 RAVICLORA 466 10 13 P.CL 624 RAVICLORA 466 10 14 P.CL 624 RAVICLORA 466 10 15 P.CL 624 RAVICLORA 466 10 16 P.CL 624 RAVICLORA 466 10 17 P.CL 624 RAVICLORA 466 10 18 P.CL 624 RAVICLORA 466 10 19 P.CL 636 ROALLOWGEL 477 11 10 P.CL 636 ROALLOWGEL 477 11 11 P.CL 636 ROALLOWGEL 478 8 12 P.CL 636 ROALLOWGEL 478 8 14 P.CL 636 ROALLOWGEL 478 8 15 P.CL 636 ROALLOWGEL 480 8 16 P.CL 636 ROALLOWGEL 480 8 17 P.CL 636 ROALLOWGEL 480 8 18 P.CL 636 ROALLOWGEL 480 8 19 P.CL 636 ROALLOWGEL 480 8 10 P	85	17	전	612	PVNRPIDWKV	449	10	0.0002			
19 P.Q. 654 QAFTESPTYKA 451 11 19 PAL 654 QAFTLIT 452 10 10 EWN 179 QAGFLIT 453 10 11 EWN 179 QAGFLIT 454 11 11 M.C 57 QAMCWAGELM 456 10 12 EWN 107 QAMCWAGELM 456 10 13 M.C 57 QAMCWAGELM 456 10 14 N.C 18 QAMCWAGELM 459 10 15 N.C 18 QAMCWAGELM 461 9 16 X 8 QLDPARDV 461 9 16 X 8 QLDPARDV 461 9 17 N.C 99 QLLWFHISCL 462 11 18 N.C 528 RAFPICLA 466 8 19 PCL 685 QVFAOATPT 465 9 10 FCL 685 QVFAOATPT 465 9 11 RAC 624 RIVGLIGFA 466 9 12 RAC 624 RIVGLIGFA 466 9 13 RAC 624 RIVGLIGFA 466 9 14 RAC 624 RIVGLIGFA 467 11 15 RAC 624 RIVGLIGFA 466 9 16 RAC 624 RIVGLIGFA 466 9 17 BW 88 ROALLWHEICH 472 11 18 N.C 56 ROALCWGELM 473 8 19 RAC 35 RIPPAYTRPNA 477 11 10 RAC 36 RVAEDLIK 478 8 11 FCL 35 RIPPAYTRPNA 478 8 12 RAC 36 RVAEDLIK 478 8 14 RAC 36 RVAEDLIK 489 9 15 RAC 36 RVAEDLIK 489 9 16 RAC 35 RVAFASPLIYA 484 9 17 RAC 35 RVAFASPLIYA 484 9 18 RAC 35 RVAFGENIYA 484 9 10 RAC 35 RVAFGENIYA 484 9 11 RAC 35 RVAFGENIYA 484 9 12 RAC 35 RVAFGENIYA 484 9 13 RAC 35 RVAFGENIYA 484 9 14 RAC 35 RVAFGENIYA 484 9 15 RAC 35 RVAFGENIYA 484 9 16 RAC 35 RVAFGENIYA 484 9 17 RAC 35 RVAFGENIYA 484 9 18 RAC 35 RVAFGENIYA 484 9 19 RAC 35 RVAFGENIYA 484 9 10 357 RVAFGENIYA 364 9 11 35 RVAFGENIYA 364	95	19	젛	654	QAFTFSPT	450	æ				
19 BW 179 OAGFFLLT 452 8 16 BW 179 OAGFFLLTRIL 453 10 16 BW 179 OAGFFLLTRIL 453 10 18 NLC 57 OALCWGELM 456 9 19 BW 107 OAMCWNSTT 456 9 16 X 8 OLDPABDY 460 8 16 X 8 OLDPABDY 461 9 17 NLC 99 OLLWHISCL 465 9 18 NLC 99 OLLWHISCL 465 9 19 PQL 685 OVEADATY 465 9 <	95		전	654	QAFTFSPTYKA	451	11				
16 BW 179 OAGFFLTRII 453 10 18 NLC 57 OAGLOWGEL 454 11 18 NLC 57 OAGLOWGEL 456 9 19 BW 107 OAMICWGEL 456 10 16 KN 107 OAMICWGEL 456 10 16 X 8 OLDPARDY 460 8 16 X 8 OLDPARDY 460 8 16 X 8 OLDPARDYC 460 9 17 NLC 99 OLLWHISCL 462 11 19 PCL 624 RIVELLARA 466 8 10 BW 18 RAVELLARA 466 8	95		&	179	QAGFFLLT	452	80				
16 BW 179 OAGFFLTRIL 454 11 18 NLC 57 OALCWGELM 455 9 18 NLC 57 OALCWGELM 456 10 19 BW 107 OAMCWMST 456 10 16 BW 107 OAMCWGELM 456 10 16 BW 107 OAMCWGELM 456 10 16 BW 107 OAMCWGELM 458 10 16 X 8 OLDPARDV 460 8 16 X 8 OLDPARDVCL 462 11 18 NC 99 OLLWHBOCL 462 11 17 NLC 99 OLLWHBOCL 465 9 19 POL 624 RAFPHCLA 466 8 19 POL 628 RAFPHCLA 466 9 10 BW 187 RILIPOSL 466 9 </td <td>80</td> <td>16</td> <td>8</td> <td>179</td> <td></td> <td>453</td> <td>10</td> <td></td> <td></td> <td></td> <td></td>	80	16	8	179		453	10				
18 NLC 57 OALCWGEL 455 9 19 NLC 57 OALCWGELM 456 10 19 NLC 17 OAMOWNSTT 457 8 16 NLC 18 OASACLCGML 459 10 16 X 8 OLDPARDVL 461 9 16 X 8 OLDPARDVCL 462 11 16 X 8 OLDPARDVCL 462 11 16 X 8 OLLWFHSCL 463 10 17 NLC 99 OLLWFHSCL 463 11 19 NLC 99 OLLWFHSCL 465 9 19 NLC 528 RAFPHCLA 466 8 19 NLC 624 RIVGILGFA 466 9 16 BN 18 RAFPHCLA 466 9 16 BN 11 465 9 10	80	16	8	179	QAGFFLTRIL	454	=				
18 NLC 57 OALCWGELM 456 10 19 BN 107 OAMOWNST 457 8 16 NLC 18 OAMOWNST 458 9 16 X 8 OLDPARDV 469 10 16 X 8 OLDPARDV 461 9 16 X 8 OLDPARDV 461 9 16 X 8 OLDPARDV 461 9 16 X 8 OLDPARDVC 462 11 17 NLC 99 OLLWHARCC 463 10 19 POL 685 OVFADATPT 465 9 19 POL 685 OVFADATPT 466 8 19 POL 684 HITIPOSL 466 9 10 BN RAFPHCLA 466 8 9 10 BN 18 RAFLIMPA 467 467 11	90	18	3	22	QAILCWGEL	455	6				
19 BW 107 OAMOWNSTT 457 8 16 NLC 18 OAMOWNSTT 458 9 16 X 8 QLDPARDVL 460 8 16 X 8 QLDPARDVL 461 9 16 X 8 QLDPARDVL 461 9 16 X 8 QLDPARDVL 461 9 18 X 8 QLDPARDVL 461 9 18 NLC 99 QLLWFHISCL 462 11 19 POL 685 QVFADATPT 465 9 19 POL 685 QVFADATPT 465 9 19 POL 624 RIVCILGFAA 466 9 18 POL 624 RIVCILGGAA 465 9 18 POL 624 RIVCILGGAA 466 9 18 N.C 56 ROALLWFHISCL 477 11 <td></td> <td>18</td> <td>3</td> <td>57</td> <td>QAILCWGELM</td> <td>456</td> <td>10</td> <td></td> <td></td> <td></td> <td></td>		18	3	57	QAILCWGELM	456	10				
16 BW 107 OAMOWNSTT 458 9 16 X 8 QLDPARDV 460 8 16 X 8 QLDPARDV 461 9 16 X 8 QLDPARDVCL 462 11 18 NLC 99 QLLWFHISCL 463 10 19 NLC 99 QLLWFHISCL 465 9 19 POL 685 QLDARDATPT 465 9 19 POL 685 QLLWFHISCL 465 9 19 POL 685 QULWFHISCL 465 9 19 POL 624 RAFPHCLA 466 8 18 POL 624 RINGLIGFAA 466 8 18 POL 624 RINGLIGFAA 466 8 18 POL 624 RINGLIGFAA 466 8 18 N.C 56 ROALLWFISCL 473	92	19	8	107	QAMQWNST	457	80				
16 NUC 18 QASKLCLGWL 459 10 16 X 8 QLDPARDVL 460 8 16 X 8 QLDPARDVL 461 9 16 X 8 QLDPARDVLCL 462 11 18 NLC 99 QLWFHISCL 463 10 17 NLC 99 QLWFHISCL 464 11 19 POL 628 RAFPHCLA 465 9 16 BW 187 RILTIPOSL 465 9 16 BW 187 RILTIPOSL 465 9 16 BW 187 RILTIPOSL 465 9 18 POL 624 RIVGLIGFAA 469 10 18 POL 56 ROAILCWGELM 472 11 18 NLC 56 ROAILCWGELM 474 11 18 NLC 56 ROAILCWGELM 475	80	16	8	107	QAMOWNSTT	458	о				
16 X 8 QLDPARDV 460 8 16 X 8 QLDPARDVL 461 9 16 X 8 QLDPARDVLCL 461 11 16 NLC 99 QLLWHISCL 463 10 17 NLC 99 QLLWHISCL 464 11 19 POL 628 QULMHISCL 465 9 19 POL 628 QULMHISCL 466 8 18 POL 624 RIVGLIGFA 466 8 18 POL 624 RIVGLIGFA 468 9 18 POL 624 RIVGLIGFA 468 9 18 POL 624 RIVGLIMPA 470 8 18 NLC 56 ROAILCWGELM 473 8 18 NLC 56 ROAILWHI 473 8 18 NLC 56 ROAILWHI 475 11	80	16	3	18	CASKLCLGWL	459	10				
16 X 8 QLDPARDVL 461 9 16 X 8 QLDPARDVLCL 462 11 18 NAC 99 OLLWFHISCL 465 10 19 POL 685 QVFADATPT 465 9 19 POL 624 RAFPHCLA 466 8 16 BNV 187 RILTIPOSL 467 9 18 POL 624 RIVGLIGFAA 468 9 18 POL 624 RIVGLIGFAA 468 9 18 POL 624 RIVGLIGFAA 468 9 18 POL 624 RIVGLIGFAA 469 10 18 POL 56 ROALCWGEL 477 11 18 NLC 56 ROALCWGEL 473 8 18 NLC 98 ROLLWFHISCL 474 11 18 NLC 38 ROALWFHISCL 475	80	16	×	ω	QLDPARDV	460	89	0.0001			
16 X 8 QLDPARDVLCL 462 11 18 NUC 99 QLUWFHISCL 463 10 17 NUC 99 QLUWFHISCLT 465 9 19 PCL 685 QVFADATPT 465 9 19 PCL 685 QVFADATPT 465 9 19 PCL 628 RAFPHCLA 466 8 16 BNV 187 RNGLIGEA 466 8 18 PCL 624 RNGLIGEA 469 10 18 PCL 106 RLKLIMPA 470 8 18 PCL 56 ROALCWGELM 471 10 18 NUC 56 ROALLWFHISCL 474 11 18 NUC 58 ROLLWFHISCL 475 11 18 NUC 353 RTPPARYTGGV 476 10 19 NUC 354 RNAFASPLHV 48	80	16	×	œ	QLDPARDVL	461	6	0.0001			
18 NUC 99 OLLWFHISCL 463 10 17 NUC 99 OLLWFHISCLT 464 11 19 PCL 685 OVFADATPT 465 9 19 PCL 628 RAFPHCLA 466 8 16 BNV 187 RILTIPOSL 467 9 18 PCL 624 RINGLIGFA 468 9 18 PCL 624 RINGLIGFA 468 9 15 PCL 106 RILKIMPA 470 10 18 NUC 56 ROAICWGEL 471 10 18 NUC 56 ROAILWFHISCL 474 11 18 NUC 98 ROLLWFHISCL 475 11 18 NUC 98 ROLLWFHISCL 475 11 19 NUC 353 RIPARATPOR 475 11 19 NUC 354 RAMEASPLHV <t< td=""><td>80</td><td>16</td><td>×</td><td>æ</td><td>QLDPARDVLCL.</td><td>462</td><td>=</td><td>0.0001</td><td></td><td></td><td></td></t<>	80	16	×	æ	QLDPARDVLCL.	462	=	0.0001			
17 NLC 99 QLLWFHISCLT 464 11 19 PQL 685 QVFADATPT 465 9 19 PQL 528 RAFPHCLA 466 8 16 BW 187 RILTIPOSL 466 9 16 BW 187 RILTIPOSL 467 9 18 POL 624 RIVGLGFAA 468 9 18 POL 624 RIVGLGFAA 469 10 18 POL 56 ROALCWGEL 470 11 18 NLC 56 ROALCWGELM 472 11 18 NLC 56 ROALLWPHI 473 8 18 NLC 98 ROLLWPHISCL 475 8 19 NLC 127 RTPPAYPENA 475 11 19 NLC 127 RTPPAYPENA 476 11 19 NLC 36 RVHEASPL 480 <td>90</td> <td>18</td> <td>3</td> <td>66</td> <td>OLLWFHISCL</td> <td>463</td> <td>. 01</td> <td>0.0060</td> <td></td> <td></td> <td></td>	90	18	3	66	OLLWFHISCL	463	. 01	0.0060			
19 POL 685 QVFADATPT 465 9 19 POL 528 RAFPHCLA 466 8 16 EW 187 RILTIPOSL 465 9 18 POL 624 RIVGLGFAA 468 9 18 POL 624 RIVGLGFAA 469 10 15 POL 106 RLKLIMPA 470 8 18 NLC 56 ROALCWGEL 471 10 18 NLC 98 ROLLWHSCL 472 11 18 NLC 98 ROLLWHSCL 474 11 17 BW 88 ROSGROPT 475 8 18 POL 353 RTPARYTGGV 476 10 19 NLC 127 RTPPAYRPNA 477 11 19 POL 36 RVAEDLNLGNL 480 8 16 POL 818 RVHFASPLHV 481	85	17	3	66	QLLWFHISCLT	464	=				
19 POL 528 RAFPHCLA 466 8 16 BNV 187 RILTIPOSL 467 9 18 POL 624 RIVGLGFAA 468 9 18 POL 624 RIVGLGFAA 469 10 15 POL 106 RLKLIMPA 470 8 18 NLC 56 ROALCWGEL 471 10 18 NLC 56 ROALCWGELM 472 11 18 NLC 98 ROLLWHI 472 11 18 NLC 98 ROLLWHISCL 474 11 17 BNV 88 ROSGROPT 475 8 18 POL 353 RTPARYTGGV 476 10 19 NLC 127 RTPARYTGGV 478 8 16 POL 818 RVHFASPL 480 8 16 POL 818 RVHFASPL 481	95	19	텇	685	QVFADATPT	465	6	0.0001			
16 BW 187 RILTIPOSL 467 9 18 POL 624 RIVGLIGFAA 468 9 18 POL 624 RIVGLIGFAA 469 10 15 POL 106 RILKLIMPA 470 8 18 NUC 56 ROALCWGEL 471 10 18 NUC 56 ROALLWHI 472 11 18 NUC 98 ROLLWHI 473 8 18 NUC 98 ROLLWHISCL 474 11 17 BW 88 ROLLWHISCL 474 11 17 BW 88 ROLLWHISCL 475 8 18 POL 35 RTPARYREGY 476 10 19 NUC 127 RTPPAYRPANA 478 8 10 POL 318 RVHFASPLHY 480 8 10 POL 818 RVHFASPLHY 481 <td>92</td> <td>19</td> <td>젒</td> <td>528</td> <td>RAFPHCLA</td> <td>466</td> <td>80</td> <td></td> <td></td> <td></td> <td></td>	92	19	젒	528	RAFPHCLA	466	80				
18 POL 624 RIVGLIGFAA 468 9 18 POL 624 RIVGLIGFAA 469 10 15 POL 106 RLKLIMPA 470 8 18 NLC 56 ROALCWGEL 471 10 18 NLC 56 ROALCWGELM 472 11 18 NLC 98 ROLLWHI 473 8 18 NLC 98 ROLLWHISCL 474 11 17 BW 88 ROLLWHISCL 474 11 17 BW 88 ROLLWHISCL 475 8 18 POL 353 RTPARVTGGV 476 10 19 NLC 127 RTPPAYRPANA 478 8 19 NLC 127 RTPARVTGGV 478 8 16 POL 818 RWHFASPLHV 480 8 15 POL 818 RWHFASPLHV 483	80	16	}	187	RILTIPOSL	467	6	0.0010			
18 PQL 624 RIVGLIGFAA 469 10 15 PQL 106 RLKLIMPA 470 8 18 NLC 56 ROALCWGEL 471 10 18 NLC 56 ROALLWHI 472 11 18 NLC 98 ROLLWHISCL 474 11 17 BW 88 ROLLWHISCL 474 11 17 BW 88 ROLLWHISCL 474 11 18 POL 353 RTPARVTGGV 476 10 19 NLC 127 RTPPAYRPNA 477 11 19 NLC 127 RTPPAYRPNA 478 8 16 POL 36 RVAEDLNI GNL 478 8 16 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHVA 481 9 20 POL 357 RYIGGVFL <td< td=""><td>06</td><td>18</td><td>점</td><td>624</td><td>RIVGLLGFA</td><td>468</td><td>6</td><td></td><td></td><td></td><td></td></td<>	06	18	점	624	RIVGLLGFA	468	6				
15 PQL 106 RLKLIMPA 470 8 18 NJC 56 ROALCWGEL 471 10 18 NJC 56 ROALLWHI 472 11 18 NJC 98 ROLLWHISCL 474 11 17 BW 88 ROLLWHISCL 474 11 17 BW 88 ROLLWHISCL 474 11 18 POL 353 RTPARVTGGV 476 10 19 NJC 127 RTPPAYRPNA 477 11 19 POL 36 RVAEDLNL 478 8 16 POL 36 RVAEDLNLGNL 479 11 15 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHVA 481 10 10 POL 818 RVHFASPLHVA 483 8 20 POL 357 RVTGGVFL 4	06	18	젙	624	RIVGLLGFAA	469	10	•			
18 NLC 56 ROALCWGEL 471 10 18 NLC 56 ROALWEIM 472 11 18 NLC 98 ROLLWHISCL 474 11 17 BW 88 ROLLWHISCL 474 11 17 BW 88 ROLLWHISCL 475 8 18 POL 353 RTPARVTGGV 476 10 19 NLC 127 RTPPAYRPNA 477 11 19 POL 36 RVAEDLNL 478 8 16 POL 316 RVAFASPL 480 8 15 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHVA 481 9 20 POL 357 RVIGGVFL 9	7.5	15	점	106	RLKLIMPA	470	89				
18 NLC 56 ROALCWGELM 472 11 18 NLC 98 ROLLWFHI 473 8 18 NLC 98 ROLLWFHISCL 474 11 17 ENV 88 ROSGRQPT 475 8 18 POL 35.3 RTPARVTGGV 476 10 19 NLC 127 RTPPAYRPPNA 477 11 19 POL 36 RVAEDLNL 478 8 16 POL 36 RVAEDLNLGNL 479 11 16 POL 818 RVHFASPL 480 8 15 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHVA 481 11 20 POL 357 RVTGGVFL 483 8 20 POL 357 RVTGGVFL 9	06	18	3	26	ROALCWGEL	471	10				
18 NLC 98 ROLLWFHI 473 8 18 NLC 98 ROLLWFHISCL 474 11 17 ENV 88 ROSGRQPT 475 11 18 POL 35.3 RTPARVTGGV 476 10 19 NLC 127 RTPPAYRPPNA 477 11 19 POL 36 RVAEDLNL 478 8 16 POL 818 RVHFASPL 480 8 15 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHVA 481 10 20 POL 357 RVTGGVFL 483 8 20 POL 357 RVTGGVFL 9	06	18	3	26	ROALCWGELM	472	11				
18 NLC 98 ROLLWFHISCL 474 11 17 BN 88 ROSGRQPT 475 8 18 POL 353 RTPARVTGGV 476 10 19 NLC 127 RTPPAYRPPNA 477 11 19 POL 36 RVAEDLNL 478 8 16 POL 818 RVHFASPL 480 8 15 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHVA 481 10 20 POL 357 RVIGGVFL 483 8 20 POL 357 RVIGGVFL 9	90	18	3	86	ROLLWFHI	473	œ				
17 BN 88 ROSGROPT 475 8 18 POL 353 RTPARVTGGV 476 10 19 NLC 127 RTPPAYRPNA 477 11 19 POL 36 RVAEDLNL 478 8 18 POL 818 RVHFASPL 480 8 15 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHVA 482 11 20 POL 357 RVIGGVFL 483 8 20 POL 357 RVIGGVFL 9	06	18	3	98	ROLLWFHISCL	474	-				
18 POL 353 RTPARVTGGV 476 10 19 NLC 127 RTPPAYRPNA 477 11 19 NLC 127 RTPPAYRPNA 477 11 18 POL 36 RVAEDLNIGNL 479 11 16 POL 818 RVHFASPL 480 8 15 POL 818 RVHFASPLHVA 481 10 15 POL 818 RVHFASPLHVA 482 11 20 POL 357 RVTGGVFL 483 8 20 POL 357 RVTGGVFL 9	82	17	2	88	ROSGROPT	475	80				
19 NLC 127 RTPPAYRPNA 477 11 19 POL 36 RVAEDLNIC 478 8 18 POL 36 RVAEDLNIGNL 479 11 16 POL 818 RVHFASPL 480 8 15 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHVA 482 11 20 POL 357 RVTGGVFL 483 8 20 POL 357 RVTGGVFL 9	06	18	점	353	RTPARVTGGV	476	10				
19 POL 36 RVAEDLNL 478 8 18 POL 36 RVAEDLNLGNL 479 11 16 POL 818 RVHFASPL 480 8 15 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHVA 482 11 20 POL 357 RVTGGVFL 483 8 20 POL 357 RVTGGVFLV 484 9	9.2	19	3	127	RTPPAYRPPNA	477	Ξ				
18 POL 36 RVAEDLNLGNL 479 11 16 POL 818 RVHFASPLHV 480 8 15 POL 818 RVHFASPLHVA 481 10 15 POL 818 RVHFASPLHVA 482 11 20 POL 357 RVTGGVFL 483 8 20 POL 357 RVTGGVFL 484 9	95	19	점	36	RVAEDLNI.	478	80				
16 POL 818 RVHFASPL 480 8 15 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHVA 482 11 20 POL 357 RVTGGVFL 483 8 20 POL 357 RVTGGVFLV 484 9	06	18	점	36	RVAEDLNLGNL	479	Ξ				
15 POL 818 RVHFASPLHV 481 10 15 POL 818 RVHFASPLHVA 482 11 20 POL 357 RVTGGVFL 483 8 20 POL 357 RVTGGVFL 9	80	16	젍	818	RVHFASPL	480	æ				
15 POL 818 RVHFASPLHVA 482 11 20 POL 357 RVTGGVFL 483 8 20 POL 357 RVTGGVFLV 484 9	7.5	15	젙	818	RVHFASPLHV	481	10	0.0001			
20 POL 357 RVTGGVFL 483 8 20 POL 357 RVTGGVFLV 484 9	7.5	15	전	818	RVHFASPLHVA	482	Ξ				
20 POL 357 RVTGGVFLV 484 9	100	20	젒	357	RVTGGVFL .	483	&				
	100	20	젍	357	RVTGGVFLV	484	6	0.0041			

Table VIII	=			HBV A02 SI	A02 SUPER MOTIF (With binding information	(With bind	ing informa	tion)			
nservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	AA	A*0201	A*0202	A.0203	A.0206	A.6802
00	a ,	>	3 9	SACBCAIBET	485	7					
ם מי	0 0	۶ ۲	520	SAICSWABBA	486	2 5	0 0001				
06		3 3	35	SALYREAL	487	2 ac					
100	20	절	9 4	SIPWTHKV	488	, α					
9.2	19	8	194	SLDSWMTSL	489	O					
7.5	15	점	565	SLGIHLNPNKT	490	Ξ					
95	19	8	337	SLLVPFVQWFV	491	Ξ					
75	15	젙	581	SLNFMGYV	. 492	80					
7.5	15	헏	581	SLNFMGYVI	493	6	0.0038				
92		×	54	SLRGLPVCA	494	6	0.0007				
06	18	절	403	SLTNLLSSNL	495	10	0.0014				
75	15	}	216	SOSPTSNHSPT	496	Ξ					
7.5	15	8	280	STGPCKTCT	497	6					
100	20	3	141	STLPETTV	498	89					
100	20	3	141	STLPETTW	499	6	0.0019				
80	16	8	85	STNROSGROPT	200	Ξ					
85	17	젍	548	SVOHLESL	501	8					
80	16	8	330	SVRFSWLSL	502	6	0.0001				
80	16	8	330	SVRFSWLSLL	503	10	0.0004				
80	16	8	330	SVRFSWLSLLV	504	=					
90	18	젍	739	SVVLSRKYT	. 505	6					
92	19	ಕ	524	SVVRRAFPHCL	206	Ξ					
85	17	젍	716	TAELLAACFA	207	01					
92	19	3	53	TALROAIL	508	æ					
80	16	3	33	TASALYREA	509	6					
80	16	3	33	TASALYREAL	510	0.					
06	18	8	190	TIPOSLDSWWT	511	=					
100	20	3	142	TLPETTVV	512	80					
100	20	전	150	TLWKAGIL	513	œ					
92	19	점	636	TOCGYPAL	514	æ					
95	19	젗	636	TOCGYPALM	515	6					
92	19	점	636	TOCGYPALMPL	516	Ξ					
85	17	ğ	798	TTGRTSLYA	517	თ					
75	15	2	278	TTSTGPCKŢ	518	თ					
7.5	15	8	278	TTSTGPCKTCT	519	=					
85	17	점	100	TVNEKRRL	520	æ					
80	16	2	16	TVQASKLCL	521	6	0.0002				
7.5	15	}	352	TVWLSVIWM	522	თ	0.0002				
92	19	점	37	VAEDLNLGNL	523	10	0.0001				
92	19	×	5	· VLCLRPVGA	524	6	0.0014				
85	17	점	543	VLGAKSVQHL	525	10	0.0001				
06	1 8	×	133	VLGGCRHKL	526	6	0.0009				

	A*6802				0.0002	0.0170																				0.0310								0.0320					0.0002				
	A.0206				0.9000	0.3400																				0.3600								0.1000					0.1000				
	A-0203				0.0210	4.9000																				7.2000								0.5600					0.0024				
tion)	A.0202				0.0001	0.2200																				0.0380								0.0005					0.0001				
ing informa	A.0201	0.0001	0.0012		0.0440	0.5800	0.0019	0.0660	0.0011									0.0003		0.0270		0.0053			0.0059	1.1000		0.0005	0.0019	0.0009	0.0001			0.0160			0.3800		0.0250				
(With bind	АА	10	6	80	O	=	6 0	တ	01	ω	=	01		80	æ	=	80	10	=	6	=	10	=	80	თ	6	80	တ	Ξ	10	တ	-	80	10	Ξ	80	o	1	6	10	80	6	10
A02 SUPER MOTIF (With binding information	SEQ ID NO:	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	260	561	562	563	564	565	566	267	568
HBV A02 S	Sequence	VLGGCRHMLV	VLHKRTLGL	VLLDYQGM	VLLDYOGML	VLLDYOGMLPV	VLOAGFFL	VLOAGFFLL	VLQAGFFLLT	VOASKLCL	VOASKLCLGWL	VOWFVGLSPT	VQWFVGLSPTV	VTGGVFLV	VVLGAKSV	WLGAKSVQHL	WLSRKYT	WARAFPHOL	VVRRAFPHCLA	WILRGTSFV	WILRGTSFVYV	WLLGCAANWI	WLLGCAANWIL	WLSLDVSA	WLSLDVSAA	WLSLLVPFV	WMCLRRFI	WMCLRRFII	WMCLARFIFL	WMMWWGPSL	WTHKVGNFT	WIHKVGNFTGL	YLHTLWKA	YLHTLWKAGI	YLHTLWKAGIL	YLPLDKGI	YLVSFGVWI	YLVSFGVWIRT	YMDDVVLGA	YOGMLPVCPL	YOHFRIAL :	YOHFRILL	YOHFRKILLL
	Position	133	92	259	259	259	177	177	177	17	17	343	343	358	542	542	740	525	525	759	759	751	751	414	414	335	237	237	237	359	25	25	147	147	147	122	118	118	538	263	S	ιΩ	rS
	Protein	×	×	}	2	}	8	}	}	3	3	₩	<u>}</u>	전	점	전	젒	젙	점	점	전	전	젙	젙	젍	2	<u>8</u>	2	≥	2	점	절	젍	전	점	점	3	3	점	}	점	점	<u>Ğ</u>
=	Frequency	18	17	19	19	18	19	19	19	16	16	19	19	20	18	16	18	19	19	16	16	16	16	50 5	19	20	19	19	19	17	20	19	20	20	20	20	18	18	18	18	15	15	15
Table VIII	Conservancy	06	85	95	95	06	98	98	95	80	80	95	95	100	06	80	06	98	95	80	80	80	80	100	95	100	95	95	95	85	100		100	100	100	100	06	06	06	06	7.5	7.5	7.5

			10. 404. 00		V AUZ SOFEN MOTIF (WILL BILIAIN) IIIOIIIIIANOI					
ુ	Protein	onservancy Frequency Protein Position Sequence	Sequence	SEQ ID NO:	AA	A.0201	A*0201 A*0202	. A*0203 A*0206 A*6802	A.0206	A.6802
	젍	746	YTSFPWLL	569	œ					
	ಕ	746	YTSFPWLLGCA	570	-					
	점	768	YVPSALNPA	571	o	0.0039				

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	MOTIF
	SUPER
	A03
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Table IX				HBV A03 S	SUPER	MOTIF	(With binding information	ling inforr	nation)				
Conservancy	Frequency	Protein	Position	Sequence	P2	term C	AA	A-0301	A.1101	A-3101	A-3301	A-6801	SEO ID NO:
85	17	ğ	721	AACFARSR	A	α	- &	0.0004	0.0003	0.0056	0.0035	0.0014	572
95	6 7	점 8	521	AICSVVRR		oc o	ω÷	-0.0002	0.0003	0.0014	-0.0009	0.0006	573
9 60 O 52	<u> </u>	₹×	7//	AL RETSAR		c 01	2 ∞	0.0003	0000	0.0450	0.0230	0.0004	575
80	9	ේ වූ	822	ASPLHVAWR	S	æ	ာတ						576
7.5	15	& 8	84	ASTNROSGR	σ.	Œ	တေ	0.0009	0.0002	0.0088	0.0008	0.0001	577
80 ec	16	ಶ ×	755 60	CARINMILH	∢ ⊲	ı a	သော	0.0034	0.0230	1 5000	0000	0 7300	8/c 8/5
06	- 60	< ×	17	CLRPVGAESR	ر _	: cc	, c	0.0011	0.0001	2	9	2	580
100	50	3	48	CSPHHTALR	S	<u>~</u>	്	0.0029	0.0001	0.0520	0.0250	0.0440	581
85	17	2	29	DLLDTASALYR	ا ب	œ (Ξ,	0.0042	-0.0003	-0.0012	3.7000	0.0410	582
80 G	<u>, , , , , , , , , , , , , , , , , , , </u>	3 5	35	DTASALYR	⊢ «	<u>ac</u> a	ω;	0.0004	-0.0002	-0.0009	0.0018	0.0009	583
ဂင္	<u>~</u> ⊂	2 2	718	FLLAACFAR	< -	c 00	_ o:	0.0003	0.0003	-0.00	200.0	0.0	585
9 60	7	ಕ್ಷ	718	ELLAACFARSR	ب ر	: œ	· =	0.0062	0.0016	0.0200	0.2000	0.1600	586
95	19	3	174	ETTWARAR	-	Œ	80	0.0003	-0.0002	-0.0009	0.1400	0.0027	587
80	16	3	174	ETTWRRRGR	- .	cc (0 9	0.0003	0.0001				588
0 0	9 0	철 >	821 53	FASPLHVAWR	∢ 0	ac o	0 0						283
) ()	o	< ₽	656	FIESPTYK	o -	c ×	2 ∝	0.0100	0.0100	0.0023	0.2100	0.0590	591
9 6 9 8	9 - 0	<u>්</u> ස්	518	FTSAICSWR	· - -	: Œ	5	0.0003	0.0003				592
95	19	젒	518	FTSAICSWAR	-	œ	11	0.0065	0.0092	0.0170	0.0350	1.5000	593
001	8 .	× {	132	PALGGCRHK Cii i sigaii	> -	××	o c	0.0430	0.0000				594
C 4	. t	₹ 8	567	ANIANTHIS ADVINGIN INIO		< '	o Ç	0 005	0 00 1	0000	0000	0000	0 0 c
75	. .	ಕ್ಷ	567	GIHLNPNKTKR		c مح	2 =	0.00	2	9		9	597
85	17	SE SE	29	GMDIDPYK	Σ	¥	60	9000.0	0.0004	-0.0009	-0.0009	0.0001	598
06		젇 8	735	GTDNSVALSR	⊢ ⊦	ac 2	. 10	0.0010	0.0420	0.0030	0.0019	0.0008	200
9 9 4	ο σ	Z Z	735	GVAVIRTPPAYR	- >	∠ α	= =	0.0140	0.3900	6 8000	0.0000	0.000	600
0 0	. 69	33	104	HISCLIFGR		: œ		0.0160	0.0065				602
7.5	15	젍	569	HLNPNKTK		¥	ω -						603
. 75	15	젇 8	569	HLNPNKTKR	4 بــ	OC 3	თ ;	0.0025	0.0001	0	9	0	604
<u> </u>	0 2	Z Z	201	ISCI TEGE	- v:	∠ Œ	_ oc	0.3400	0.4400	0.0370	0.07	0.1900	609 606
100	20	전	153	KAGILYKR	✓	œ	, c o	0.0002	-0.0002	0.0015	-0.0009	0.0001	607
80	16	젙	610	KLPVNRPIDWK	ب	¥	Ξ						809
75		×	130	KVFVLGGCR	> -	oc 0	o (0.0420	0.0820	0.009	0.0710	0.0030	609
n C	- 4	₹ 2	719	I AACEAR	< _	c a	n oc	0.0038	0.0003	0.0015	0.0029	0.0064	9 10
8 8 2	17	<u></u>	719	LLAACFARSR	نـ ،	. cc	5						612
82	17	3	30	LLDTASALYR	_ .	<u>م</u> ر	0	0.0050	0.0002				613
80	9 4	<u></u>	752	LLGCAANWILH	ں ب	I Y	<u>.</u> :						615
0 c	. 0	3	169	LSTLPETTWR	ာ ဟ	< œ	- +-	-0.0009	0.0008	-0.0012	-0.0023	0.0078	616
7.5	15	ಕ	က	LSYOHFRK	ဟ	¥	80						617
85	17	ಕ :	66	LTWNEKRR	- :	<u>د</u> (&	-0.0002	-0.0002	-0.0009	-0.0009	0.0001	618
06	18	38	911	LVSFGVWIR	> >	ro	ñ -	0.0028	0.0120	0.0260	0.020	0.4900	919
75	15	ź×	103	MSTTDLEAYFK	> W	x	2 =			0.0400	0.63.0	200	621
06	8	3	7.5	NLEDPASR	_	Œ	80	-0.0002	-0.0002	-0.0009	-0.0009	0.0001	622

	SEQ ID NO:	623	624 635	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	944	0 40	740	648	649	650	651	652	653	654	000	657	658	629	099	661	662	663	664	665	999	299	999	669	0/0	672	673	
	.A•6801	0.0019	0.000	0.000	0.000	0.000			0.0001	0.0001	0.0005	0.0001	0.0002	0.0002	0.0009	1.2000				0.0005		6.1000	0.0003		0000	0.0003	0.0001	0.0360	0.0690	0.3800	0.0003	0036.0	0.750	0.3100			0.0590	0.0180	0.0440	0.6400	0.0130	0.0640	0.0820	0.0048	0.0170	3000	0.00		
	A-3301	-0.0023	-0.003	0.00	0.00	0.0			-0.0009	-0.0009	0.0008	-0.0009	0.0027	0.0043	9000.0	0.0057				0.0490		1.2000	-0.0023		0 00 14	0.0016	-0.0003	0.0024	0.0081	0.0650	-0.0023	0091	0.1600	0.1600			0.1600	0.0024	0.0120	0.0710	0.0010	0.1100	0.0200	0.0066	0.0012	0 110	2		
	A:3101	-0.0012	-0.003	0.000	0.00	0.0.0			-0.0009	-0.0009	0.0006	-0.0009	0.0004	0.0004	0.0002	0.0010				3.1000	0	2.6000	0.0.30		0.0033	0.2000	-0.0002	0.0029	0.0280	0.1500	-0.0012	0000	0.3300	0.1000			9900'0	0.0009	0.0006	0.0061	0.0051	0.1000	0.0600		0.0006	0 2500	0.63.0		
nation)	A.1101	0.0005	0.00.0		0.000	0.0002	0.0005		-0.0002	-0.0002	0.0031	-0.0002	0.0005	0.0005	0.1400	0.5400				0.0005	0	3.8000	-0.0003		-0.000	0.0005	0.0290	0.0020	0.0071	0.2100	-0.0003	0077	0.400	1,4000		2.7000	0.0023	0.0002	0.0230	0.0160	0.3600	0.0095	0.0008	0.0006	0.9200	3000	0.000		,
ding inform	A.0301	-0.0009	0.0000	0.0020	0.000	0.000	00000		0.0002	-0.0002	0.0011	0.0002	0.0008	0.0002	0.0310	0.0450				0.0950		0.2800	7000.0-		0000	0.0054	0.0190	-0.0002	-0.0002	0.0058	-0.0004	000	0.0080	0.0150		0.0066	9000'0	0.0008	0.0007	0.0005	5.3000	0.0082	0.0005	0.0018	0.0006	9000	0.000		
MOTIF (With binding information)	AA	Ξ,	no d	n c	na	» C	? o	o ac	, c c	, α	, 0 ,	8	o	6	6	0	o	-	æ	o (Ξ;	= ;	_ 0	0 0	ກ∝	o 01	Ξ	80	89	6	Ξ:	2 -	» ÷	2 =	œ	10	Ξ	თ	0 :	Ξ	0	Ξ	თ	<u>.</u> 5	തം	o c	n oc	· =	
MOTIF	C. term	× ;	۷ ک	۵ د	c a	c œ	: ac	: ×	. oc	æ	×	œ	œ	œ	¥	¥	œ	Œ	Œ	ac (ac (x c	c o	د ۵	ב מ	: cc	*	œ	Œ	Œ	œ :	∠ 0	c 0	: a:	œ	¥	œ	œ	oc (œ	∠ (oc i	œ	nc :	× >	< 0	coc	: 00	:
SUPER	P2	_ (n >	> <	(<	< ∢	: -		ب .	· _	_	_	_	>	>	∢	∢	S	တ	_ .	.	ه د	n u	n u	o F		>	⋖	⋖	∢	∢ .	ں <u>ر</u>	ი ⊢	- 1-	-	-	∢	_	. لىــ	_		٠ د	တ	so I	⊢ ⊦	- -	- >	· >	
HBV A03 S	Sequence	NENVSIPWITH	NSVVLSHN	acacacaca	מילי גינסעם	PASTNROSGR	PIDWAYCOR	PIII GFRK	PLEEBPR	PLSYOHER	PLSYCHFFIX	PLTWNEKR	PLTVNEKAR	PVGAESRGR	PVNRPIDWK	QAFTFSPTYK	OAGFFLLTR	OSPRARRSOSR	OSSGILSR	RLKLIMPAR	RUKVFVLGGCR	HCVVO-WO-WA	DOOCOODD	addagood	RESPER	RTPSPRRR	RVTGGVFLVDK	SAGPCALR	SAICSVVR	SAICSVVRR	SALNPADDPSR	SCGINCNENS	STANTONIA STANTONIA	STLPETTWER	STINFOSGR	STTDLEAYFK	TAELLAACFAR	TLPETTWR	TUPETTWIRE	TLPETTWARR	TLWKAGILYK	TLWKAGILYKR	TSAICSVVR	TSAICSWAR	TTDLEAYFK	מסממיארד	TWARAGE	TWARAGASPR	
	Position	45	/ 3B	776	? ;	- c	616	496	20	5	ι α	98	98	20	612	654	179	169	189	106	128	376	103	167	188	188	357	65	520	520	771	565 64	4 o +	170	85	104	716	171	171	171	150	150	519	519	105	2/8	176	176	:
	Protein	#	₹8	2 2	<u>ځ</u> >	< ₹	2	2	<u></u>	ğ	점	ਬ	젙	×	전	점	₩	3	젍	ත් :	×į	₹;	3 2	3 2	3 <u>c</u>	2	ಕ	×	ಕ್ಷ	절	젇 :	₫,	< <u>-</u>	3 3	8	×	젍	3	2	2	<u>ಕ</u>	<u></u>	<u>ğ</u>	전 :	× č	≥ C D Z	3 2	2	<u>!</u>
	Frequency	6 9	0 C	0 4	0 4	- -		. 4	9 6	20	15	17	17	. 18	17	19	16	15	16	5 .	5 .	5 6	. T	n 4		9 6	50.	18	19	19	8 :		0 0	9 6	16	15	17	19	19	19	20	20	- 6	6.	to t		<u> </u>	9 4	:
Table IX	Conservancy	S 6) F	8	9 6	90	. o	0 6	9 69	100	75	85	85	06	85	95	80	7.5	80	7.5	75	ຄ	n 4	0 4	0 o	9 6	100	06	95	92	06	c 6) u	n 47	80	1 75	85	95	95	92	100	100	95	S 6	75	n (0 6	80	1

Table IX				HBV A03 S	UPER	MOTIF	HBV A03 SUPER MOTIF (With binding information)	g inform	nation)				
Conservancy Frequency	Frequency	Protein	Position	Sequence	P2	C- merm	АА	A.0301	A-1101	A*1101 A*3101	A.3301	A*6801	SEQ ID
06	18	×	133	VLGGCRI I K		¥	80	0.0150	0.0002	-0.0005	-0.0009	0.0001	674
80	16	8	177	VLOAGFFILTR	_	œ	=						675
06	18	3	120	VSFGVWIR	တ	Œ	80	0.0040	0.0290	0.0750	0.0270	0.0360	919
100	20	ಕ	48	VSIPWTHK	တ	×	œ	0.0130	0.0170	0.0031	0.0013	0.0004	677
100	20	헏	358	VTGGVFLVDK	_	¥	5	0.0390	0.0920	0.0002	9000.0	0.0022	678
100	20	절	378	WDFSQFSR	>	œ	Ø	0.0015	0.0750	0.0013	0.0170	0.0330	619
80	16	3	177	WARAGRSPR	>	œ	10	0.0027	0.0001				680
80	16	3	177	WARRGRSPAR	>	œ	Ξ						681
95	19	3	125	WIRTPPAYR	-	œ	6	0.0008	0.0005				682
06	18	젍	314	WLOFFINSK	_	¥	. 00	-0.0002	0.0005	0.0020	0.0052	0.0001	683
82	17	3	56	WLWGMDIDPYK	_	¥	=	0.0030	0.0013	.0.0003	0.0039	0.0490	684
100	20	8	122	YLPLDKGIK	_	¥	6	0.0001	0.0001	0.0006	9000.0	0.0002	685
06	18	3	118	YLVSFGVWIR	_	œ	01	0.0005	0.0002				989
06	18	헏	538	YMDDVVLGAK	₹	¥	10	0.0330	0.0043	0.0002	9000.0	0.0001	687
80	16	ğ	493	YSHPIILGFR	ဟ	œ	10						688
80	16	젍	493	YSHPIILGFRK	ဟ	×	=						689

Conse	rvancy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID NO
	95	19	POL	529	AFPHCLAF	XFXXXXXF		690
	95	19	POL	529	AFPHCLAFSY	XFXXXXXXXY		691
	95	19	POL	529	AFPHCLAFSYM	XFXXXXXXXXX		692
	95	19	×	62	AFSSAGPCAL	XFXXXXXXXL	0.0012	693
	90	18	POL	535	AFSYMDDVVL	XFXXXXXXXL	0.0009	694
	95 95	19 19	POL	655	AFTFSPTY AFTFSPTYKAF	XFXXXXXXY		695 696
	95	19	POL POL	655 521	AICSVVRRAF	XFXXXXXXXXF XIXXXXXXXXF		697
	90	18	NUC	58	AILCWGEL	XIXXXXXL		698
	90	18	NUC	58	AILCWGELM	XIXXXXXXM		699
	95	19	POL	642	ALMPLYACI	XLXXXXXXI		700
	95	19	NUC	54	ALRQAILCW	XLXXXXXXW		701
	80	16	EW	108	AMOWNSTTF	XMXXXXXXF		702
	95	19	POL	690	ATPTGWGL	XTXXXXXL		703
	75	15	POL.	690	ATPTGWGLAI	XTXXXXXXXI		704
	95	19	POL	397	AVPNLQSL	XVXXXXXL		705
	95	19	POL	397	AVPRICALING	XVXXXXXXXXL	0.0260	706
	100 100	20 20	NUC NUC	131 131	AYRPPNAPI AYRPPNAPIL	XYXXXXXXXI XYXXXXXXXL	0.0260	707 708
	75	15	POL	607	CFRKLPVNRPI	XFXXXXXXXXXXI	0.0220	709
	100	20	BW	312	CIPIPSSW	XIXXXXXXW		710
	100	20	BW	312	CIPIPSSWAF	XIXXXXXXXF		711
	85	17	NUC	23	CLGWLWGM	XLXXXXXM		712
	85	17	NUC	23	CLGWLWGMDI	XLXXXXXXXI		713
	100	20	₽W	253	CLIFLLVL	XLXXXXXL		714
	100	20	EW.	253	CLIFLLVLL	XLXXXXXXL		715
	95	19	EW.	253	CLIFLLVLLDY	XLXXXXXXXXY		716
	95	19		239	CLRRFIIF	XLXXXXXF		717
	95	19	₽W	239	CLRRFIIFL	XLXXXXXXL		718
	75	15	EW.	239	CLRRFIIFLF	XLXXXXXXF		719
	75	15	BW	239	CLRRFIIFLFI	XLXXXXXXXXI		720
	100	20	BW SW	310	CTCIPIPSSW DIDPYKEF	XTXXXXXXXW	•	721 722
	90 85	18 17	NUC NUC	31 29	DLLDTASAL	XIXXXXXF XLXXXXXXXL		723
	85	17	NUC	29	DLLDTASALY	XLXXXXXXXXY		724
	95	19	POL	40	DLNLGNLNVSI	XLXXXXXXXXI		725
	80	16	NUC	32	DTASALYREAL	XTXXXXXXXXL		726
	85	17	POL	618	DWKVCQRI	XWXXXXXI		727
	85	17	POL	618	DWKVCQRIVGL	XWXXXXXXXXL		728
	90	18	EW.	262	DYQGMLPVCPL	XYXXXXXXXXL	0.0002	729
	80	16	×	122	ELGEEIRL	XLXXXXXL		730
-	95	19	NUC	43	ELLSFLPSDF	XLXXXXXXXF		731
	95	19	NUC	43	ELLSFLPSDFF	XLXXXXXXXXF		732
	90	18	NUC	117	EYLVSFGVW	XYXXXXXXXW	0.0040	733
	90 100	18 20	NUC	117	EYLVSFGVWI FFCLWVYI	XYXXXXXXXI	0.0340	734 735
	80	16	BW BW	382 182	FFLLTRIL	XFXXXXXI XFXXXXXL		736
	80	16	BW	182	FFLLTRILTI	XFXXXXXXXXI		737
	85	17	EW	13	FFPDHQLDPAF	XFXXXXXXXXXX		738
	80	16	EW.	243	FIIFLFIL	XIXXXXXL		739
	80	16	EW	243	FIIFLFILL	XIXXXXXXL		740
	80	16	EW	243	FIIFLFILLL	XIXXXXXXXL		741
	80	16	. EW	248	FILLLCLI	XIXXXXXI	-	. 742
	80	16	E//	248	FILLLCLIF	XIXXXXXXF	•	743
	80	16	E/V/	248	FILLLCLIFL	XIXXXXXXXL		744
	80	16	E/W	248	FILLLCLIFLL	XIXXXXXXXXL		745
	80	16	E/V	246	FLFILLLCL	XLXXXXXXL		746
	80	16	EW.	246	FLFILLLCLI	XLXXXXXXXI		747
	80 75	16 15	BW	246	FLFILLLÖLIF FLGPLLVL	XLXXXXXXXXF		748 749
	75 95	15 19	POL	171 513	FLLAQFTSAI	XLXXXXXL XLXXXXXXXI		749 750
	95	19	POL	562	FLLSLGIHL	XLXXXXXXXL		751
	80	16	BW	183	FLLTRILTI	XLXXXXXXI		752
	95	19	₽₩	256	FLLVLLDY	XLXXXXXY		753
	95	19	₽W	256	FLLVLLDYQGM	XLXXXXXXXXM		754
	95	19	POL	656	FTFSPTYKAF	XTXXXXXXXF		755
	95	19	POL	656	FTFSPTYKAFL	XTXXXXXXXXL		756
	95	19	POL	635	FTQCGYPAL	XTXXXXXXL		757
	95	19	POL .	635	FTQCGYPALM	XTXXXXXXXM		758
	95	19	EW.	346	FVGLSPTVW	XVXXXXXXW		759
	95	19	₽W	346	FVGLSPTVWL	XVXXXXXXXL		760
	90	18	×	132	FVLGGCRHKL	XVXXXXXXXL		761
	95	19	₽W	342	FVQWFVGL	XVXXXXXL		762
	90	18	POL	766	FVYVPSAL	XVXXXXXL		763
	95	19	POL	630	GFAAPFTQCGY	XFXXXXXXXXXY		764
	80	16	EW.	181	GFFLLTRI	XFXXXXXI		765
	80	16	EW EW	181	GFFLLTRIL	XFXXXXXXL		766 767
	80 95	16	BW BW	181	GFFLLTRILTI	XFXXXXXXXXXXI		767 768
	95 75	19 15	EW EW	12	GFFPOHOL GFLGPLLVL	XFXXXXXL		768 769
	75 80	16	POL	170 500	GFRKIPMGVGL	XFXXXXXXXL XFXXXXXXXXXL		769 770
	95	19	POL	627	GLLGFAAPF	XLXXXXXXXX	· 	770

Conservancy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID NO:
100	20	BW	348	GLSPTVWL	XLXXXXXL		773
75	15	₽ W	348	GLSPTVWLSVI	XLXXXXXXXXI		774
85	17	NUC	29	GMDIDPYKEF	XMXXXXXXXF		775
90 90	18 18	BW POL	265	GMLPVCPL GTDNSVVL	XMXXXXXL		776
75	15	BW	735 13	GTNLSVPNPL	XTXXXXXL XTXXXXXXXL		777 778
80	16	POL	763	GTSFVYVPSAL	XTXXXXXXXXL		779
80	16	POL	507	GVGLSPFL	XVXXXXXL		780
80	16	POL	507	GVGLSPFLL	XVXXXXXXL		781
95	19	NUC	123	GVWIRTPPAY	XVXXXXXXXY		782
· 85	17 17	NUC NUC	25 25	GWLWGMDI GWLWGMDIDPY	XWXXXXXXI		783 784
85	17	BW	65	GWSPQAQGI	XWXXXXXXI	0.0024	785
. 85	17	BW.	65	GWSPQAQGIL	XWXXXXXXXL	0.0003	786
95	19	POL	639	GYPALMPL	XYXXXXXL		787
95	19	POL.	639	GYPALMPLY	XYXXXXXXXY	0.0490	788
95	19	BW.	234	GYRWMCLRRF	XYXXXXXXXF	0.0110	789
95 85	19 17	EW POL	234 579	GYRWMCLRRFI GYSLNFMGY	XYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	0.0002	790 791
75	15	POL	579	GYSLNFMGYVI	XYXXXXXXXXI	0.0002	792
80	16	POL	820	HFASPLHVAW	XFXXXXXXXW		793
75	15	POL	7	HFRKLLLL	XFXXXXXXL		794
80	16	POL	435	HLLVGSSGL	XLXXXXXXL		795
75	15	POL	569	HLNPNKTKRW	XLXXXXXXXW		796
80	16	POL	491	HLYSHPII	XLXXXXXI		797
80 80	16 16	POL *	491 491	HLYSHPIIL HLYSHPIILGF	XLXXXXXXL XLXXXXXXXXF		798 799
85	17 -		715	HTAELLAACF	XTXXXXXXXF		800
100	20	NUC	52	HTALRQAI	XTXXXXXI	•	801
95	19	NUC	52	HTALRQAIL	XTXXXXXXL		802
95	19	NUC	52	HTALRQAILCW	XTXXXXXXXXX		803
100	20	POL.	149	HTLWKAGI	XTXXXXXI		804
100 100	20 20	POL	149	HTLWKAGIL HTLWKAGILY	XTXXXXXXL		805
100	20	POL POL	149 146	HYLHTLWKAGI	XTXXXXXXXY XYXXXXXXXXI		806 807
100	20	BW	381	IFFCLWVY	XFXXXXXY		808
100	20	EW	381	IFFCLWVYI	XFXXXXXXI	0.0087	809
80	16	EW	245	IFLFILLL	XFXXXXXL		810
. 80	16	EW.	245	IFLFILLLCL	XFXXXXXXXL		811
80	16	BW	245	IFLFILLLCLI	XFXXXXXXXXI		812
95 80	19 16	EW EW	255 244	IFLLVLLDY IIFLFILL	XFXXXXXXY XIXXXXXL		813 - 814
80	16	BW	244	HFLFILLL	XIXXXXXXL		815
80	16	BW	244	HFLFILLLCL	XIXXXXXXXXL		816
80	16	POL	497	IILGFRKI	XIXXXXXI		817
80	16	POL	497	IILGFRKIPM	XIXXXXXXXIX		818
90	18	NUC	59	ILCWGELM	XLXXXXXM		819
80 100	16 20	POL	498	ILGFRKIPM	XLXXXXXXM		820
100	20	BW BW	249 249	ILLLCLIF ILLLCLIFL	XLXXXXXF XLXXXXXXL		821 822
100	20	BW	249	ILLLCLIFLL	XLXXXXXXXL		823
80	16	POL	760	ILRGTSFVY	XLXXXXXXY		824
95	19	₽₩	188	ILTIPOSL	XLXXXXXL	•	825
90	18	₽W	188	ILTIPOSLDSW	XLXXXXXXXXW	•	826
90	18	POL	625	IVGLLGFAAPF	XVXXXXXXXXF	0.0004	827
85 95	17 19	EW POL	358 3 95	IWMMWYWGPS KFAVPNLQSL	XWXXXXXXXXL XFXXXXXXXL	0.0004 0.0020	828 829
80	16	POL	503	KIPMGVGL	XIXXXXXL	0.0020	830
80	16	POL	503	KIPMGVGLSPF	XIXXXXXXXXF		831
85	17	NUC	21	KLCLGWLW	XLXXXXXW		832
85	17	NUC	21	KLCLGWLWGM	XLXXXXXXXM		833
95	19	POL	489	KLHLYSHPI	XLXXXXXXI		834
80	16	POL.	489	KLHLYSHPII	XLXXXXXXXI		835
80 75	16 15	POL POL	489 108	KLHLYSHPIIL KLIMPARF	XLXXXXXXXL XLXXXXXF		836 837
75 75	15	POL.	108	KLIMPARFY	XLXXXXXXY		838
80	16	POL.	610	KLPVNRPI	XLXXXXXI		839
80	16	POL	610	KLPVNRPIDW	XLXXXXXXXW		840
95	19	POL .	574	KTKRWGYSL	XTXXXXXXL		841
85	17	POL	574	KTKRWGYSLNF	XTXXXXXXXXF		842
85 85	17	POL	620	KVCQRIVGL	XVXXXXXXL		843
85 95	17 19	POL POL	620 55	KVCQRIVGLL KVGNFTGL	XVXXXXXXL XVXXXXXL		844 845
95	19	POL	55 55	KVGNFTGLY	XVXXXXXXXX		846
85	17	X	91	KVLHKRTL	XVXXXXXL		847
85	17	x	91	KVLHKRTLGL	XVXXXXXXXL		848
100	20	POL	121	KYLPLDKGI	XYXXXXXXI	0.0028	849
85	17	POL	745	KYTSFPWL	XYXXXXXL		850
85	17	POL	745	KYTSFPWLL	XYXXXXXXL	3.6000	851
	16	₽₩	247	LFILLLCL	XFXXXXXL		852
80					VEVVVVV		050
80 80 80	16 16	EW EW	247 247	LFILLLCLI LFILLLCLIF	XFXXXXXXI XFXXXXXXXF	•	853 854

Conservancy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID NO:
100	20	BW	254	LIFLLVLL	XIXXXXXL		856
95	19	BW	254	LIFLLVLLDY	XIXXXXXXXXY		857
100	20	POL	109	LIMPARFY	XIXXXXXY		858
95	19	POL	514	LLAQFTSAI	XLXXXXXXI		859
100 100	20 20	BW BW	251	LLCLIFLL LLCLIFLLVL	XLXXXXXL		860 861
100	20	EW EW	251 251	LLCLIFLLVLL	XLXXXXXXXXL XLXXXXXXXXXL		862
85	17	NUC	30	LLDTASAL	XLXXXXXL		863
85	17	NUC	30	LLDTASALY	XLXXXXXXXY		864
95	19	₽W	260	LLDYQGML	XLXXXXXL		865
. 80	16	POL.	752	LLGCAANW	XLXXXXXW		866
80 80	16 16	POL POL	752 752	LLGCAANWI LLGCAANWIL	XLXXXXXXXI XLXXXXXXXXL		867 868
95	19	POL	628	LLGFAAPF	XLXXXXXXF		869
75	15	BW	63	LLGWSPQAQGI	XLXXXXXXXXI		870
100	20	₽W	250	LLLCLIFL	XLXXXXXL		871
100	20	₽W	250	LLLCUFLL	XLXXXXXXL		872
100 100	20 20	BW	250	LLLCLIFLLVL LLPIFFCL	XLXXXXXXXXXL		873 874
100	20	BW BW	378 378	LLPIFFOLW	XLXXXXXXL XLXXXXXXXW		875
100	20	BW	378	LLPIFFCLWVY	XLXXXXXXXXY		876
95	19	NUC	44	LLSFLPSDF	XLXXXXXXF		877
95	19	NUC	44	LLSFLPSDFF	XLXXXXXXXF		878
95	19	POL	563	LLSLGIHL	XLXXXXXL		879
90 90	18 18	POL POL	407 407	LLSSNLSW LLSSNLSWL	XLXXXXXXW XLXXXXXXXL		880 881
90	18	POL	407	LLSSNLSWLSL	XLXXXXXXXXL		882
80	16	BW.	184	LLTRILTI	XLXXXXXI		883
. 80	16	POL	436	LLVGSSGL	XLXXXXXL		884
95	19	BW.	257	LLVLLDYQGM	XLXXXXXXXM		885
95 95	19 19	BW BW	257 175	LLVLLDYQGML LLVLQAGF	XLXXXXXXXXL XLXXXXXF		886 887
95	19	BW.	175	LLVLQAGFF	XLXXXXXXF		888
90	18	EW.	175	LLVLQAGFFL	XLXXXXXXXL		889
90	18	EW.	175	LLVLQAGFFLL	XLXXXXXXXXL		890
100	20	BW.	338	LLVPFVQW	XLXXXXXW		891
100 90	20 18	NUC ENV	338 100	LLVPFVQWF LLWFHISCL	XLXXXXXXF XLXXXXXXL		892 893
85	17	NUC	100	LLWFHISCLTF	XLXXXXXXXXX		894
95	19	POL	643	LMPLYACI	XMXXXXXI		895
75	15	NUC	137	LTFGRETVL	XTXXXXXXL		896
75	15	NUC	137	LTFGRETVLEY	XTXXXXXXXXY		897
90 90	18 18	EW.	189	LTIPQSLDSW LTIPQSLDSWW	XTXXXXXXXXW		898 899
90	18	POL	189 404	LTNLLSSNL	XTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		900
90	18	POL	404	LTNLLSSNLSW	XTXXXXXXXXW		901
80	16	₽ V V	185	LTRILTIPOSL	XTXXXXXXXXL		902
85	17	POL.	99	LTVNEKRRL	XTXXXXXXL		903
95 95	19 19	EW/	258	LVLLDYQGM LVLLDYQGML	XVXXXXXXM		904 905
95	19	EW EW	258 176	LVLQAGFF	XVXXXXXXXXL XVXXXXXF		906
90	18	BW/	176	LVLQAGFFL	XVXXXXXXL		907
90	18	₽ V V	176	LVLQAGFFLL	XVXXXXXXXL	_	908
100	20	B∕v∨	339	LVPFVQWF	XVXXXXXF	- · · · · · · · · · · · · · · · · · · ·	909
95 90	19	BW	339	LVPFVQWFVGL LVSFGVWI	XVXXXXXXXXL		910
100	18 20	NUC POL	119 377	LVVDFSQF	XVXXXXXI XVXXXXXF		911 912
90	18	NUC	101	LWFHISCL	XWXXXXXXL		913
85	17	NUC	101	LWFHISCLTF	XWXXXXXXXF		914
85	17	NUC	27	LWGMDIDPY	XWXXXXXXY		915
100	20	POL CC	151	LWKAGILY	XWXXXXXY		916
80 80	16 16	POL POL	492 492	LYSHPIIL LYSHPIILGF	XYXXXXXXL XYXXXXXXXXF	1.1000	917 918
85	17	BW	360	MMWYWGPSL	XMXXXXXXL	0.0012	919
85	17	BW	360	MMWYWGPSLY	XMXXXXXXXY	0.0001	920
85	17	BW.	361	MWYWGPSL	XWXXXXXL		921
85	. 17	BW.	361	MWYWGPSLY	XWXXXXXXY	0.0027	922
95	19	POL.	561	NFLLSLGI	XFXXXXXI	0.0000	923
95 95	19 19	POL POL	. 561 42	NFLLSLGIHL NLGNLNVSI	XFXXXXXXXL XLXXXXXXXI	0.0099	924 925
95	19	POL	42	NLGNLNVSIPW	XLXXXXXXXXX		926
90	18	POL	406	NLLSSNLSW	XLXXXXXXW		927
90	18	POL	406	NLLSSNLSWL	XLXXXXXXXL		928
95	19	POL	45	NLNVSIPW	XLXXXXXW		929
100	20	POL.	400	NLQSLTNL NLOSLTNL	XLXXXXXL		930
100 75	20 15	POL BW	400 15	NLOSLTNLL NLSVPNPL	XLXXXXXXL XLXXXXXXL		931 932
75 75	15	BW	15	NLSVPNPLGF	XLXXXXXXXXF		932
80	16	POL	758	NWILRGTSF	XWXXXXXXF		934
80	16	POL	758	NWILRGTSFVY	XWXXXXXXXXX		935
95	19	POL	512	PFLLAQFTSAI	XFXXXXXXXXI	2.222	936
95 95	19 19	POL POL	634 634	PFTQCGYPALM	XFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	0.0002	937 938
90	13	74	034	TT TOO TEALM	AF************************************		330

Table X	_	<u>n.</u>	•	SUPER MO		and moniation)	
Conservancy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID NO:
95	19	BW	341	PFVQWFVGL	XFXXXXXXL	0.0003	939
85	17	POL.	616	PIDWKVOQRI	XIXXXXXXII		940
100	20	BW.	380	PIFFCLWVY	XIXXXXXXY		941
100 85	20 17	ENV POL	380 713	PIFFCLWVYI PIHTAELL	XIXXXXXXXI		942 943
80	16	POL	496	PIILGFRKI	XIXXXXXXXI		944
80	16	POL	496	PIILGFRKIPM	XIXXXXXXXXM		945
100	20	BW	314	PIPSSWAF	XIXXXXXF		946
100	20	POL	124	. PLDKGIKPY	XLXXXXXXY		947
100	20	POL	124	PLDKGIKPYY	XLXXXXXXXY		948
95	19	POL	20	PLEERLPRL	XLXXXXXXL		949
95	19	₽ ₩	10	PLGFFPDHOL PLHPAAMPHL	XLXXXXXXXL		950
, 100 100	20 20	POL POL	427 427	PLHPAAMPHLL	XLXXXXXXXXL XLXXXXXXXXXL		951 952
100	20	EW.	377	PLLPIFFCL	XLXXXXXXXL		953
100	20	BW.	377	PLLPIFFCLW	XLXXXXXXXXW		954
95	19	₽₩	174	PLLVLQAGF	XLXXXXXXF		955
95	19	₽₩	174	PLLVLQAGFF	XLXXXXXXXF		. 956
90	18	BW.	174	PLLVLQAGFFL	XLXXXXXXXXL		957
80	16	POL	711	PLPIHTAEL	XLXXXXXXL		958
80 75	16 15	POL POL	711 2	PLPIHTAELL PLSYQHFRKL	XLXXXXXXXXL XLXXXXXXXXXL		959 960
75 75	15	POL	2	PLSYQHFRKLL	XLXXXXXXXXL		961
85	1,7	POL	98	PLTVNEKRRL	XLXXXXXXXL		962
80	16	POL	505	PMGVGLSPF	XMXXXXXXF		963
80	16	POL -	505	PMGVGLSPFL	XMXXXXXXXL		964
80	16	POL	505	PMGVGLSPFLL	XMXXXXXXXXL		965
75	15	POL	692	PTGWGLAI	XTXXXXXI		966
85 85	17 17	POL.	797 707	PTTGRTSL PTTGRTSLY	XTXXXXXL		967 968
80	16	POL NUC	797 15	PTVQASKL	XTXXXXXXY XTXXXXXL		969
80	16	NUC	15	PTVQASKLCL	XTXXXXXXXL	•	970
75	15	BW	351	PTVWLSVI	XTXXXXXI		971
75	15	₽W	351	PTVWLSVIW	XTXXXXXXW		972
75	15	EW.	351	PTVWLSVIWM	XTXXXXXXM		973
85	17	POL	612	PVNRPIDW	XVXXXXXW		974
80 80	16 16	POL POL	750 750	PWLLGCAANWI PWLLGCAANWI	XWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		975 976
100	20	POL	51	PWTHKVGNF	XWXXXXXXF	0.0290	977
80	16	×	8	QLDPARDVL	XLXXXXXXL	5.5255	978
80	16	×	8	QLDPARDVLCL	XLXXXXXXXXL		979
90	18	NUC	99	OLLWFHISCL	XLXXXXXXXL		980
95	19	POL	685	QVFADATPTGW	XVXXXXXXXXX		981
95 75	19 15	BW 8W	344 242	QWFVGLSPTVW RFIIFLFI	XWXXXXXXXX		982 983
75 75	15	. BW	242	RFIIFLFIL	XFXXXXXXXL		984
75	15	BW	242	RFIIFLFILL	XFXXXXXXXL		985
75	15	EW	242	RFIIFLFILLL	XFXXXXXXXXL		986
100	20	₽W	332	RFSWLSLL	XFXXXXXL		987
100	20	BW.	332	RFSWLSLLVPF	XFXXXXXXXXF		988
80 90	16	₽W	187	RILTIPOSL RIVGLLGF	XIXXXXXXL		989 990
75	18 15	POL POL	624 106	RLKLIMPARF	XIXXXXXF XLXXXXXXXF		991
75	15	POL	106	RUKLIMPARFY	XLXXXXXXXXY	•	992
95	19	POL	376	RLWDFSQF	XLXXXXXXF	·	993
90	18	POL	353	RTPARVTGGVF	XTXXXXXXXXF		994
95	19	POL	36	RVAEDLNL	XVXXXXXL		995
90	18	POL.	36	RVAEDLNLGNL	XVXXXXXXXL		996
80 100	16 20	POL.	818 357	RVHFASPL RVTGGVFL	XVXXXXXL		997 998
85	17	POL POL	357 577	RWGYSUNF	XVXXXXXL XWXXXXXF		999
85	17	POL	577	RWGYSLNFM	XWXXXXXXXM		1000
85	17	POL	577	RWGYSLNFMGY	XWXXXXXXXXY		1001
95	19	EW.	236	RWMCLRRF	XWXXXXXF		1002
95	19	₽W.	236	RWMCLRRFI	XWXXXXXXI	0.0710	1003
95	19	BW.	236	RWMCLRRFII	XWXXXXXXXI	1.1000	1004
95	19	₽ ₩	236	RWMCLRRFIIF SFCGSPYSW	XWXXXXXXXXF	0.0710	1005
100 95	20 19	POL NUC	167 46	SFLPSDFF	XFXXXXXXW XFXXXXXF	0.0710	1006 1007
80	16	POL	765	SFVYVPSAL	XFXXXXXXXL		1007
100	20	POL	49	SIPWTHKVGNF	XIXXXXXXXXF		1009
95	19	BW	194	SLDSWWTSL	XLXXXXXXL		1010
95	19	₽W	194	SLDSWWTSLNF	XLXXXXXXXXF		1011
95	19	POL	416	SLDVSAAF	XLXXXXXF		1012
95	19	POL	416	SLDVSAAFY	XLXXXXXXY		1013
100 100	20 20	BW BW	337	SLLVPFVQW SLLVPFVQWF	XLXXXXXXW		1014 1015
75	15	ENV POL	337 581	SLNFMGYVI	XLXXXXXXXF XLXXXXXXXI		1016
95	19	X	54	SLRGLPVCAF	XLXXXXXXXXF		1017
90	18	PÔL.	403	SLTNLLSSNL	XLXXXXXXXL		1018
75	15	x	104	STTDLEAY	XTXXXXXY		1019
75	15	×	104	STTDLEAYF	XTXXXXXXF		1020
75	15	B/V	17	SVPNPLGF	XVXXXXXF		1021

85 17 PCL 548 SVAPEANE, XYODOOCK, 1023 80 16 8 PCL 330 SVAPEANE, XYODOOCK, 1023 80 16 8 PCL 330 SVAPEANE, XYODOOCK, 1023 80 16 8 PCL 330 SVAPEANE, XYODOOCK, 1028 80 17 PCL 524 SVAPEANE, XYODOOCK, 1028 80 17 PCL 524 SVAPEANE, XYODOOCK, 1028 80 18 PCL 322 SVAPEANE, XYODOOCK, 1028 80 18 PCL 322 SVAPEANE, XYODOOCK, 1028 80 18 PCL 322 SVAPEANE, XYODOOCK, 1028 80 19 PCL 323 SVAPEANE, XYODOOCK, 1028 80 19 PCL 32	Conservancy	Freq	Protein	Position	Sequence	String		A*2401	SEQ ID NO:
80	85		POL	548	SVQHLESL	XVXXXXXL			1022
90							•	•	
85 17 POL 739 SYNLSPINTS XY00000000F 1026 95 19 POL 524 SYNRSPINTS XY00000000T 1027 95 19 POL 192 SYNRSPINTS XW0000000T 1027 195 19 POL 192 SYNRSPINTS XW000000T 1020 195 19 POL 192 SYNRSPINTS XW000000T 1020 195 19 POL 192 SYNRSPINTS XW000000T 1020 195 19 POL 192 SYNRSPINTS XW00000T 1020 195 19 POL 195 SYNRSPINTS XW00000T 1020 195 195 SYNRSPINTS XW00000T 1020 195 195 SYNRSPINTS XW00000T 1020 195 SYNRSPINTS XW0									
95 19 PQL \$24 SWARPFPICEL XVDOCOCOCOCUL 1028 100 20 BW 314 SWALDLYPF XVDOCOCOCUL 0.3900 1028 100 20 BW 314 SWALDLYPF XVDOCOCOCUL 0.3900 1028 101 20 BW 314 SWALDLYPF XVDOCOCUL 0.3900 1029 101 101 SWARPFICEL XVDOCOCUL 0.3900 1021 102 SWARPFICEL XVDOCOCUL 0.3900 1021 103 SWARPFICEL XVDOCOCUL 0.3900 1023 104 SWARPFICEL XVDOCOCUL 0.3900 1023 105 S									
95 19 POL									
100 20 BN 334 SMELLUFF 0.3900 1029 95 18 PQ 392 SWPREAVIPIN XWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX									
100				334		XWXXXXXXF		0.3900	
95 19 BW 197 SWMTSL/FL XWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX								5.6000	
90 18 PCL 537 SYMDOVYL XYXXXXXXI 1033 755 15 PCL 4 SYCHFRILL XYXXXXXXI 1034 757 15 PCL 4 SYCHFRILL XYXXXXXXI 1035 757 15 PCL 4 SYCHFRILL XYXXXXXXI 1035 758 15 PCL 4 SYCHFRILL XYXXXXXXI 1036 759 15 NLC 138 TFGRIPM. XYXXXXXXI 1038 750 15 NLC 138 TFGRIPM. XYXXXXXXI 1038 751 15 NLC 138 TFGRIPM. XYXXXXXXI 1038 751 15 NLC 138 TFGRIPM. XYXXXXXI 1038 752 15 NLC 138 TFGRIPM. XYXXXXXI 1038 753 15 PCL 657 TFSFTYXAF, XYXXXXXI 1038 754 15 PCL 657 TFSFTYXAF, XYXXXXXI 1038 755 15 NLC 138 TFGRIPM. XYXXXXXI 1038 757 15 NLC 138 TFGRIPM. XYXXXXXI 1038 757 15 NLC 138 TFGRIPM. XYXXXXXI 1038 758 15 PCL 657 TFSFTYXAF, XYXXXXXI 1038 759 18 BY 190 750 18 BY 190 750 18 BY 190 750 18 BY 190 750 15 X 105 TLWXXXII XXXXXXXI 1038 751 15 NLC 138 TFGRIPM. XYXXXXXI 1038 751 15 NLC 138 TFGRIPM. XYXXXXXI 1038 752 15 NLC 138 TFGRIPM. XYXXXXXI 1038 753 15 NLC 138 TFGRIPM. XYXXXXXI 1038 754 15 NLC 138 TFGRIPM. XYXXXXXI 1038 755 15 NLC 138 TFGRIPM. XXXXXXI 1038 755 15 NLC 138 TFGRIPM. XXXXXXXI 1038 757 15 NLC 138 TFGRIPM. XXXXXXXI 1038 757 15 NLC 138 TFGRIPM. XXXXXXXI 1038 757 15 NLC 138 TFGRIPM. XXXXXXXXI 1038 757 15 NLC 138									
75 15 PCL 4 SYOFFRIL MYDOCOCIL 0.0051 1035 75 15 PCL 4 SYOFFRIL MYDOCOCIL 0.0051 1035 75 15 PCL 4 SYOFFRIL MYDOCOCIL 0.0050 1038 75 15 NCC 138 TGREPL MYDOCOCIL 0.0050 1038 75 15 NCC 138 TGREPL MYDOCOCIL 0.0050 1038 75 15 NCC 138 TGREPL MYDOCOCIL 0.0050 1039 75 15 NCC 138 TGREPL MYDOCOCIL 0.0050 1039 75 15 NCC 138 TGREPL MYDOCOCIL 0.0050 1039 75 15 NCC 138 TGREPL MYDOCOCIL 0.0050 1040 95 19 PCL 657 TFSFTYAR MYDOCOCIL 0.0060 1041 95 19 PCL 657 TFSFTYAR MYDOCOCIL 0.0060 1041 96 18 BW 190 TFSSLDSWW MYDOCOCIL 0.0060 1041 100 20 PCL 150 TLWRAGIL MYDOCOCIL 0.0060 1041 100 20 PCL 150 TLWRAGIL MYDOCOCIL 0.0060 1041 75 15 X 105 TIMEAS MYDOCOCIL 0.0060 1041 80 16 N.C 16 TWASSLC MYDOCOCIL 0.0060 1041 80 16 N.C 16 TWASSLC MYDOCOCIL 0.0060 1041 80 16 N.C 16 TWASSLC MYDOCOCIL 0.0060 1041 75 15 MYDOCOCIL 0.0060 1041 75 15 MYDOCOCIL 0.0060 1041 80 16 N.C 16 TWASSLC MYDOCOCIL 0.0060 1041 75 15 MYDOCOCIL 0.0060 1041 75 15 MYDOCOCIL 0.0060 1041 80 16 N.C 16 TWASSLC MYDOCOCIL 0.0060 1051 80 16 N.C 16 TWASSLC MYDOCOCIL 0								0.3800	
75 15 POL									
75								0.0051	
75 15 NUC 138 TFGRETM. XPROCOCK. 1038 75 15 NUC 138 TFGRETM. XPROCOCK. 1039 75 15 NUC 138 TFGRETM. XPROCOCK. 1039 75 15 NUC 138 TFGRETM. XPROCOCK. 1040 95 19 PQL 657 TFSFTYKAF. XPROCOCK. 0.0060 1041 95 19 PQL 657 TFSFTYKAF. XPROCOCK. 0.0060 1041 100 20 PQL 150 TFSFTYKAF. XPROCOCK. 0.0063 1044 100 20 PQL 150 TFWAGNI. XUCK. 1046 75 15 X 105 TFWAGNI. XUCK. 1046 75 15 X 105 TFWAGNI. XUCK. 1046 85 17 PQL 798 TGRISL. XPROCOCK. 1046 85 17 PQL 100 TFWAGNI. XUCK. 1046 85 17 PQL 100 TFWAGNI. XUCK. 1046 85 17 PQL 100 TWAGNI. XUCK. 1046 85 17 PQL 106 SEC. XUCK. 1046 85 17 PQL 106 SEC. XUCK. 1046 85 17 PQL 107 S					SYQHFRKLLL				
75 15 NUC 138 TFGRETMEY XPOCOCOCCY 1040 95 19 PCL 657 TFSPTYKAF XPOCOCOCCOCC 1040 95 19 PCL 657 TFSPTYKAF XPOCOCCOCC 1040 95 19 PCL 657 TSSPTYKAF XPOCOCCOCC 1040 95 19 PCL 150 TLWAGGIL XLXCOCCC 1040 100 20 PCL 150 TLWAGGIL XLXCOCCC 1040 100 20 PCL 150 TLWAGGIL XLXCOCCC 1040 85 17 PCL 798 TTGHTSLY XXXCOCC 1047 85 17 PCL 798 TTGHTSLY XXXCOCC 1047 85 17 PCL 798 TTGHTSLY XXXCOCC 1040 85 17 PCL 160 TWGSPL XXXCOCC 1040 86 17 NUC 100 TWGSPL XXXCOCC 1040 87 TS 15 BW 352 TWMSYW XXCOCCC 1040 87 TS 15 BW 352 TWMSYW XXCOCCC 1040 97 TS 15 BW X 153 TWMSYW XXCCCC 1040 97 TS 15 BW X 153 TWMSYW XXCCCC 1040 97 TS 15 BW X 153 TWMSYW XXCCCC 1040 97 TS 15 BW X 153 TWMSYW XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 15 BW X 154 TWMSYM XXCCCC 1040 97 TS 154 TWMSYM XXCCCC 1040 97 TS 154 TWMSYM XXCCCC 1040 97 TS 154 TWMSYM XXCCCC 1040 97 T									
75 15 N.C 138 TFGRETNLENL XPROCOCCUL 1040 1041									
95 19 POL 657 TESPTYKAF KPOCOCCK 0.0060 1041 96 19 POL 657 TESPTYKAF KPOCOCCK 0.0043 1042 90 18 BW 190 TROSLDSW XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX									
95								0.0060	
90					TFSPTYKAFL				
100						XIXXXXXXW			
100									
75									
85									
85									
16									
75									
75									
95 19 POL 686 VFADATPTGW XFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX									
75								0.0180	
90									
85 17						XLXXXXXXXL			
95 19 BW 259 VLIDYOGM XLXXXXXXX 1066 95 19 BW 177 VLOAGFT XLXXXXXXX 1066 95 19 BW 177 VLOAGFT XLXXXXXXX 1066 95 19 BW 177 VLOAGFT XLXXXXXXX 1062 85 17 PCL 741 VLSRKYTSF XLXXXXXXX 1062 85 17 PCL 741 VLSRKYTSF XLXXXXXXX 1064 80 16 PCL 741 VLSRKYTSF XLXXXXXXX 1065 85 17 PCL 740 VLSRKYTSF XLXXXXXXX 1065 85 17 PCL 740 VLSRKYTSF XLXXXXXXX 1065 95 19 PCL 525 VPRAFPHC XYXXXXXXXX 1067 95 19 NLC 124 VWIRTPAY XVXXXXXXX 1067 95 19 NLC 124 VWIRTPAY XVXXXXXXX 1069 90 18 NLC 102 VPHISCLTF XXXXXXXXX 1069 91 18 NLC 102 VPHISCLTF XXXXXXXXX 1071 95 19 BW 345 VFVGLSPTVW XFXXXXXXX 1071 95 19 BW 345 VFVGLSPTVW XFXXXXXXX 1072 80 16 PCL 759 WLRGTSF XIXXXXXXX 1073 80 16 PCL 759 WLRGTSF XIXXXXXXX 1073 80 16 PCL 759 WLRGTSF XIXXXXXXX 1073 80 16 PCL 751 WLLGCAANW XLXXXXXXX 1076 80 16 PCL 751 WLLGCAANW XLXXXXXXX 1076 80 16 PCL 751 WLLGCAANW XLXXXXXXX 1076 80 16 PCL 751 WLLGCAANW XLXXXXXXX 1077 80 16 PCL 751 WLLGCAANW XLXXXXXXX 1077 80 16 PCL 751 WLLGCAANW XLXXXXXXX 1077 80 16 PCL 751 WLLGCAANW XLXXXXXXXX 1077 80 16 PCL 751 WLLGCAANW XLXXXXXXX 1077 80 177 WACLREIF XXXXXXXXXX 10020 85 19 PCL 414 WLSLDYSAAF XLXXXXXXXX 10020 85 19 PCL 414 WLSLDYSAAF XLXXXXXXXX 10020 85 19 BW 237 WMCLREIF XMXXXXXXXX 10020 86 19 BW 335 WLSLLYPF XLXXXXXXXX 10020 87 108 BW 335 WLSLLYPF XLXXXXXXX 10020 88 17 BW 237 WMCLREIF XMXXXXXXX 10020 89 19 BW 237 WMCLREIF XMXXXXXXX 10020 85 19 BW 237 WMCLREIF XMXXXXXXX 10020 86 17 BW 359 WMMWYWGPS XMXXXXXXX 10020 87 108 BW 359 WMMWYWGPS XMXXXXXXX 10020 86 17 BW 359 WMMWYWGPS XMXXXXXXX 10020 87 109 BW 351 PRV 359 WMMWYWGPS XMXXXXXXX 10020 80 100 20 PCL 147 YLHTLWAGIL XLXXXXXXX 10020 80 18 NLC 118 VLYFGW XLXXXXXXX 10020 80 18 NL									
95 19 BW 259 NLDYGML XLXXXXXL 1066 95 19 BW 177 VLQAGFFL XLXXXXXL 1061 95 19 BW 177 VLQAGFFL XLXXXXXL 1063 85 17 PQL 741 VLSRKYTSF XLXXXXXXX 1063 85 17 PQL 741 VLSRKYTSF XLXXXXXXX 1065 85 17 PQL 740 VLSRKYTSFW XLXXXXXXX 1065 85 17 PQL 740 VLSRKYTSFW XLXXXXXXX 1065 85 19 PQL 525 VMFRAFPLC XXXXXXXXX 1067 95 19 NLC 124 VMRTFPAY XMXXXXXX 1067 95 19 NLC 124 VMRTFPAY XMXXXXXX 1069 90 18 N.C 102 VMHISCLTF XFXXXXXXX 1069 90 18 N.C 102 VMHISCLTF XFXXXXXXX 1072 80 16 PQL 759 VMLRGTSFY XIXXXXXX 1072 80 16 PQL 759 VMLRGTSFY XIXXXXXX 1072 80 16 PQL 759 VMLRGTSFY XIXXXXXX 1076 80 16 PQL 751 VMLGCAANWI XLXXXXXXX 1076 80 16 PQL 751 VMLGCAANWI XLXXXXXXX 1077 80 178 PQL 414 VMSLDVSAAF XLXXXXXXX 1078 80 16 PQL 751 VMLGCAANWI XLXXXXXXX 1078 95 19 PQL 414 VMSLDVSAAF XLXXXXXXX 1088 95 19 BW 335 VMSLLVPF XLXXXXXXX 1088 95 19 BW 237 VMCLRFIIF XMXXXXXX 1088 95 19 BW 237 VMCLRFIIF XMXXXXXX 1088 85 17 BW 359 VMMWYMGPSL XMXXXXXX 1092 85 19 BW 237 VMCLRFIIF XMXXXXXX 1092 85 17 BW 359 VMMWYMGPSL XMXXXXXX 1092 85 17 BW 359 VMMWYMGPSL XMXXXXXX 1092 85 19 BW 237 VMCLRFIIF XMXXXXXX 1092 85 19 BW 237 VMCLRFIIF XMXXXXXX 1092 85 19 BW 237 VMCLRFIIF XMXXXXXX 1092 85 17 BW 359 VMMWYMGPSL XMXXXXX 1092 85 19 BW 362 VMPMSPSL XMXXXXXX 1092 85 17 BW 359 VMMWYMGPSL XMXXXXX 1092 85 19 BW 362 VMPMSPSL XMXXXXXX 1092 85 19 BW 362 VMPMSPSL XMXXXXXX 1092 85 19 BW 362 VMPMSPSL XMXXXXXX 1092 86 17 BW 362 VMPMSPSL XMXXXXXX 1092 87 19 BW 237 VMCLRFIIF XMXXXXXX 1092 86 17 BW 369 VMMWYMGPSL XMXXXXX 1092 87 19 BW 362 VMPMSPSL XMXXXXX 1092 87 19 BW 362 VMPMSPSL XMXXXXX 1									
95 19 EN 177 VLOAGFFL XLXXXXXL 1062 85 17 POL 741 VLSRKYTSF XLXXXXXX 1062 85 17 POL 741 VLSRKYTSF XLXXXXXX 1063 85 17 POL 741 VLSRKYTSF XLXXXXXXX 1064 80 16 POL 542 VVLOAKSVOHL XVXXXXXXX 1068 95 19 POL 740 VVLSRKYTSF XXXXXXXXXX 1068 95 19 POL 525 VVFRAFPHCL XVXXXXXXXX 1067 95 19 POL 124 VVINTPPAY XVXXXXXXXX 1068 75 15 EN 353 VVLSVYM XXXXXXXX 1069 90 18 NUC 102 WFHISCLTF XFXXXXXXXX 1071 95 19 EN 345 WFVGLSFTVX XFXXXXXXX 1071 95 19 EN 345 WFVGLSFTVX XFXXXXXXX 1071 80 16 POL 759 WILRGTSFYY XIXXXXXXX 1071 95 19 NUC 125 WIRTPPAY XIXXXXXXXY 1072 80 16 POL 759 WILRGTSFYY XIXXXXXXXY 1073 80 16 POL 751 WLLGCAANW XLXXXXXY 1076 80 16 POL 751 WLLGCAANW XLXXXXXXX 1077 80 16 POL 751 WLLGCAANW XLXXXXXXX 1077 80 16 POL 751 WLLGCAANW XLXXXXXXX 1077 80 177 NUC 26 WIRTPPAY XLXXXXXXX 1077 80 19 EN 335 WLSLVPFVGW XLXXXXXXX 1082 81 10 20 EN 335 WLSLVPFVGW XLXXXXXXX 1082 81 10 EN 237 WMCLRFIEI XMXXXXXX 10001 81 10 20 EN 335 WLSLVPFVGW XLXXXXXXX 10001 81 10 20 EN 335 WMCLRFIEI XMXXXXXX 10001 81 10 EN 237 WMCLRFIEI XMXXXXXX 10001 81 10 EN 237 WMCLRFIEI XMXXXXXX 10001 81 10 20 POL 122 WHXMFYEPSL XMXXXXXX 10001 81 10 20 POL 122 WHXMFYEPSL XMXXXXXX 10001 81 10 20 POL 147 YLFTWKGRI XLXXXXXXX 10001 81 10 20 POL 147 YLFTWKGRI XMXXXXXX 10001 81 100 20 POL 147 YLFTWKGRI XMXXXXXX 10001 81 100 20 POL 147 YLFTWKGRI XMXXXXXX 100001 81 100 20									
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HBV B07 SUPER MOTIF (With binding information)

B'5401 SEQIDNO	1101		0.0093 1104	1106	1107	1108	0.0001					0.0199 1115	0.0480 1116	1117		1118		0.0035 1120 0.0002 1121																						
B*5301 B*S	0000		0.0003 0.00				0 000 0					0.5400 0.01	0.0790 0.04					0.0002 0.00 0.0001 0.00																						
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B*5101	0.0019	3	0.0004				0 0001	0.0019			0.0003	0.0665	0.0900				0.00	0.0001	0.0001 0.0002 0.0001	0.0001 0.0002 0.0001 0.0110	0.0001 0.0002 0.0001 0.0110	0.0000 0.0000 0.0001 0.0010	0.0000 0.0000 0.0001 0.0000 0.0000 0.0001	0.0001 0.0002 0.0001 0.0110 0.0002 0.0001 0.3100 0.0110	0.0001 0.0002 0.0001 0.0011 0.0002 0.0001 0.3100	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.0000 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000	0.0001 0.0002 0.0001 0.0011 0.0001 0.3100 0.0110 0.0019	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000	0.000 0.000 0.000 0.000 0.000 0.001 0.000 2.35(0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000	0.0000 0.000110 0.00110 0.000110 0.00110 0.00110 0.00110 0.00110 0.00110	0.0001 0.0001 0.0011 0.0011 0.0001 0.0110 0.0019 2.3500 0.0360	0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000	0.0000 0.00011 0.00110 0.00010 0.3100 0.0110 0.0019 2.3500 0.00000	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.0001 0.0001 0.0011 0.0001 0.0001 0.0019 2.3500 0.0360 0.0002	0.00000 0.00001 0.00011 0.00011 0.00011 0.00011 0.00001 0.00001 0.00002 0.00002 0.00002	0.0000 0.00011 0.00011 0.00011 0.00011 0.00011 0.00011 0.00002 0.00002 0.00002 0.00002
B*3501	0.0012	0.0001	0.0010				0 0001	0.0001			0.0016	0.5250	0.2200				0.0001	0.0001	0.0001	0.0001 0.0001 0.0001	0.0001 0.0001 0.0001 0.0001	00.000000000000000000000000000000000000	0.0000000000000000000000000000000000000	0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0004	0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0027 0.0027	0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0027 0.0027	0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001	0.0001 0.0001 0.0001 0.0001 0.0001 0.0004 0.0020 0.0020 0.0020	0.0001 0.0001 0.0001 0.0001 0.0001 0.0004 0.0020 0.0020 0.0020	0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0004 0.00004 0.00004 0.00004	0.0001 0.0001 0.0001 0.0001 0.0001 0.0000 0.0027 0.0027 0.0020 0.0027 0.0027 0.0027 0.0027	0.0001 0.0001 0.0001 0.0001 0.0001 0.0000 0.0027 0.0027 0.0020 0.0027 0.0027 0.0027 0.0027	0.0001 0.0001 0.0001 0.0001 0.0001 0.0004 0.0270 0.0020 0.0024 0.0020 0.0024	0.0001 0.0001 0.0001 0.0001 0.0001 0.0004 0.0027 0.0020 0.	0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0004 0.0020 0.0020 0.0020 0.0020 0.0020 0.0020 0.0020 0.0020 0.0020 0.0020 0.0020	0.0001 0.0001 0.0001 0.0001 0.0001 0.0004 0.0270 0.0020 0.0024 0.	0.0001 0.0001 0.0001 0.0001 0.0001 0.0004 0.0004 0.0004 0.0004 0.0004 0.0007 0.0001	0.0001 0.0001 0.0001 0.0001 0.0001 0.0004 0.0004 0.0004 0.0004 0.0007 0.0001 0.0001 0.0001	0.0001 0.0001 0.0001 0.0001 0.0001 0.0004 0.0020	0.0001 0.0001 0.0001 0.0001 0.0001 0.0004 0.0020
B.0702	0000	0.0029	0.2300		•		0.0120	0.0001			0.0002	0.0001	0.0990				0.0900	0.0900	0.0900 0.0001 -0.0002	0.0900 0.0001 -0.0002 0.0003	0.0900 0.0001 -0.0002 0.0003	0.0900 0.0001 0.0002 0.0003 0.0001	0.0900 0.0001 -0.0002 0.0003 0.0001 0.0011	0.0900 0.0001 -0.0002 0.0003 0.0011 0.0650 0.0650	0.0900 0.0001 -0.0002 0.0003 0.0011 0.0650 0.0980	0.0900 0.0001 -0.0002 0.0003 0.0011 0.0650 0.0980	0.0900 0.0001 0.0003 0.0001 0.0011 0.0650 0.0980 0.0160	0.0900 0.0001 0.0002 0.0003 0.0001 0.0031 0.0980 0.0980 0.0980 0.0160	0.0900 0.0001 0.0003 0.0003 0.0001 0.0031 0.0650 0.0980 0.0980 0.01300	0.0900 0.0001 0.0003 0.0001 0.0011 0.0031 0.0650 0.0980 0.01300 0.0004	0.0900 0.0001 0.0003 0.0001 0.0001 0.0650 0.0650 0.01300 0.01300	0.0900 0.0001 0.0003 0.0001 0.0001 0.0650 0.0650 0.01300 0.01300	0.0900 0.0001 0.0003 0.0003 0.0001 0.0031 0.0055 0.0980 0.0160 0.0130 0.0130 0.0130	0.0900 0.0001 0.0003 0.0003 0.0001 0.0055 0.0980 0.0130 0.0130 0.0013 0.00013	0.0900 0.0001 0.0003 0.0003 0.0001 0.0031 0.0055 0.0980 0.0130 0.0130 0.0013	0.0900 0.0001 0.0003 0.0003 0.0001 0.0055 0.0058 0.0130 0.0013 0.00013	0.0900 0.0001 0.0003 0.0001 0.0001 0.0055 0.0058 0.0058 0.0013 0.00013 0.00013	0.0900 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0002 0.0002	0.0900 0.0001 0.0001 0.0001 0.0001 0.0003 0.0003 0.0003 0.00013 0.00013 0.0002 0.0002	0.0900 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0002 0.0002 0.0002
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Sequence	APCNFFTSA	APFTOCGYPA	APFTOCG	CPTVQASKL	CPTVQAS	DPARDVLCL DPRVBG V	DPSRGRLG	DPYKEFGA	FPAGGSSSGTV	FPDHOLDPA	FPDHOLL	FPHCLAFSY	FPHCLAFSYM	FPWLGCA	EPWLLGCAA	****	GPCALRE	GPCALRFTSA GPLEEB.PRL	GPCALRFTSA GPLEEBPRL GPLEEBPRLA	GPCALRFTS GPLEEBPRI GPLEEBPRI GPLULOA	GPCALRFTSA GPCEEDPRL GPLEEDPRLA GPLVLOA GPLVLOAGF	GPCALRTSA GPCEEDPRL GPLEEDPRLA GPLYLOA GPLYLOA GPLYLOAGF GPLYLOAGF	GPCALRTSA GPLEEDPRL GPLEEDPRA GPLVLOA GPLVLOAGF GPLVLOAGF GPLVLOAGF GPLTNNEKRRL HPAAMPHIL	GPCALRETSA GPCALRETSA GPLEEBPRU GPLYLOA GPLYLOAGF GPLYLOAGF GPLYNOAGF GPLYNOAGF GPLYNOAGF GPLYNOAGF HPAAMPHLL	GPCALFTSA GPCEEDPRA GPLETORA GPLVLOA GPLVLOAGF GPLVOAGF GPLVNEKRRL HPAAMPHLL HPAAMPHLLV	GPCALLOCAN GPCALLACA GPLALOA GPLALOAG GPLALOAG GPLYLOAG GPLYLOAG GPLYNEKRF HPAAMPHL HPAAMPHL HPAAMPHLL	GPCALRTS GPCALRTS GPCALRTS GPLVLOA GPLVLOAG GPLVLOAG GPLVLOAG GPLVNEKRF HPAAMPHL HPAAMPHL HPAAMPHL HPIGFRKI IPIPSSWA	GPCALRTS GPCALRTS GPCEEDPR GPLVLOA GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVNEGR HPAAMPHL HPAA	GPLEBY GPLEBY GPLVL GPLVL GPLVL GPLVL GPLVL GPLVL GPLVNE HPAAMP HPAAMP HPRAMP H	GPCALFTSA GPCEBPRA GPLENCA GPLUNCA GPLUNCAGF GPLUNCAGF GPLUNCAGF GPLUNCAGF GPLUNCAGF GPLUNCAGF GPLUNCAGF GPLUNCAGF GPLUNCAGF GPLUNCAGF GPLUNCAGF IPPSSWA IPPSSWA IPPSSWA IPPSSWA IPPSSWA IPPSSWA IPPSSWAFA IPMGVGLSPF	GPCALRTS GPCALRTS GPCALRTS GPLULOA GPLULOAGI G	GPCALRTS GPCALRTS GPCALRTS GPLVLOA GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG HPAAMPHLL HPAA	GPCALRTSA GPLEEDPRA GPLENCOAGF GPLVLOAGF GPLVLOAGF GPLVLOAGF GPLVNEKGRL HPAAMPHLL HPAAMPHLL HPAAMPHLL HPAAMPHLL HPAAMPHLL HPASSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA IPISSWA	GPCALRTS GPCARTS GPCARTS GPCARTS GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG HPAAMPHL HPAAMP	GPCALRTS GPCALRTS GPCALRTS GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVNEKRF HPAAMPHL HP	GPCEED PRIA GPCEED PRIA GPCEED PRIA GPLYLOA GPLYLOAGF GPLYLOAGF GPLYLOAGF GPLYNOAGF GPLYNOAGF GPLYNOAGF GPLYNOAGF GPLYNOAGF GPLYNOAGF HPAAMPHLL HP	GPCALRTISA GPCALRTISA GPCEED PRA GPLEEB PRA GPLYLOA GPLYLOAGF GPLYLOAGF GPLYLOAGF GPLYLOAGF GPLYNEKRRH HPAAMPHLLV HPIACGFRI IPIPSSWAF IPIPSSWAF IPOSLOSW IPO	PAGED PR GPCALRTS GPCALRTS GPCANCOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVNEXB HPAAMPHL HPAAMPH IPFCLW LPIFFCLW LPIFFCLW LPIFFCLW LPIFFCLW LPIFFCLW	GPCALRTS GPCALRTS GPCALRTS GPCALRTS GPCALVOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG GPLVLOAG HPAAMPHL IPFCLW LPIFFCLW LPIFFCLW LPIFFCLW LPIFFCLW LPIFFCLW	GPLEBPRA GPLEBPRA GPLEBPRA GPLVLOA GPLVLOAGF GPLVLOAGF GPLVLOAGF GPLVLOAGF GPLVLOAGF GPLVLOAGF GPLVLOAGF GPLVLOAGF GPLVNEKRRL HPAAMPHL HPAAMPHL HPAAMPHL HPAAMPHL HPAAMPHL HPAAMPHL HPAAMPHL HPAAMPH HPAAMPH HPAAMPH HPAAMPH HPAAMPH HPAAMPH HPAAMPH HPAAMPH HPA
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HBV B07 SUPER MOTIF (With binding information)

SEQIDINO	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196
B.5401	0.0002	0.0001	19.0000				0.0190		0.0001	0.0001			0.0003	0.0001	0.0002	0.0002		0.0002	0.0001	0.0011	0.0093	12.0500	0.0035	0.0002						,	0.0002	0.0015	0.0006	0.000	0.00				0.1100	0.0025	0.0002	0.0002	1.0000	0.0015	0.0056	16.0000	0.0700
B*5301	0.0003	0.0007	0.0009				0.0370		-0.0003	0.0028			0.0002	-0.0003	0.0003	0.0001		0.0002	-0.0003	-0.0003	0.0009	-0.0003	0.0002	0.0005							0.0002	0.0001	0.0099	0.0005	0.0002				0.0002	0.0001	0.0001	-0.0003	0.0002	0.0001	0.0450	0.0140	0.0320
B*5101	0.0002	0.0001	0.0110				0.0120		0.0001	0.0001			0.0001	0.0001	0.0001	0.0035		0.0280	0.0018	0.0001	0.0180	0.0001		0.0004							0.0019	0.0013	0.0001	0.000					19.0000	0.0100	0.0004	0.0001	0.0070	0.0015	0.4100	0.0340	0.0470
B*3501	0.0290	0.0009	0.0710				0.0097		0.0001	0.0021	=		0.0001	0.0001	0.0002	0.0001		0.0001	0.0001	0.0001	0.0009	0.0001	0.0001	0.0001							0.0001	0.0001	0.1000	0.0001	1000.0				0.0001	0.0001	0.0001	0.0001	0.0001	0.0002	0.2600	0.0480	0.0001
B*0702	0.0001	-0.0002	0.0480				0.0001		0.0120	0.0012			0.0001	0.0003	0.0001	0.0001		0.0076	0.1300	-0.0002	0.5500	0.0820	0.0012	0.5800							0.3900	0.0078	0.3200	0.0950	0.0001				0.0010	0.0011	0.0006	0.0004	0.0011	0.0054	0.0004	0.0180	0.0040
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Sequence	LPLDKGIKPY	LPLDKGIKPYY	LPVCAFSSA	LPVNRPIDW	LPVNRPIDWKV	MPHILVGSSGL	MPLSYQHF	MPLSYQHFRKL	NPADDPSRGRL	NPLGFFPDHOL	NPNKTKRW	NPNKTKRWGY	PPAYRPPNA	PPAYRPPNAPI	PPHGGLLGW	PPNAPILSTL	RPIDWKVCQRI	RPPNAPIL	RPPNAPILSTL	SPEHCSPHHTA	SPFLLAQF	SPFLLAOFTSA	SPHHTALROA	SPHHTALROAI	SPOAGGIL	SPSVPSHL	SPTVMLSV	SPTVWLSVI	SPTVMLSVIW	SPTVWLSVIWM	SPTYKAFL	TPARVTGGV	TPARVIGGVE	I PARVIGOVEL	TENTREMA	TPPHGGL	TPTGWG! A	TPTGWGLAI	VPFVQWFV	VPFVQWFVGL	VPNLOSLTNL	VPNLOSLTNLL	VPSALNPA	WPKFAVPNL	YPALMPLY	YPALMPLYA	YPALMPLYACI
Position	123	123	58	611	611	433	-	-	774	6	571	57.1	129	129	58	134	615	133	133	44	511	511	49	49	29	808	350	350	350	350	629	354	354	354	871	رد 73	691	691	340	340	398	398	769	393	640	640	640
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Conservancy Frequency Protein	20	20	19	16	16	16	50	15	18	19	15	15	19	19	17	20	16	20	20	20	19	19	20	20	17	17	15	15	15	15	19	18	18	80 ·	5 1	<u>.</u> +	. 4	- -	6 -	19	19	19	18	19	19	19	19
Conservance	100	100	95	80	80	80	100	7.5	06	95	7.5	7.5	95	95	85	100	80	100	100	100	95	95	100	100	85	85	7.5	7.5	7.5	7.5	92	06	06	90				75	. o	95	95	9.2	06	95	9.2	95	92

SeqID Num Conservancy % Sequence Frequency HBV B27 Super Motif (No binding data available) No. of Amino Acids Position in HBV LROALCW
LRRFIIRNKTKRWGY
NRPVAEDL
PHCLAFSY
PHGGLIGW
PKFAVPNL
QHFRQULGW
RWAFPHCL
RHYLLLW
RRAFPHCL
RRFIIR-F
SHRIIGF
SKLCGW
SRNLYVSL GRETVLEYL HHTALROAI HKVGNFTGL IHTAELLAA DKGIKPYY FHISCLTF FRKIPMGV GRETVLEY HHTALRQA IHTAELLA UHKRTLGL UHLYSHPI LRGLPVCA LRGTSFVY TRHYLHTL VRFSWLSL WKVOORIV YRPPNAPI ARVTGGVFL **EHCSPHIHTA CRWGYSLNF** LHLYSHPII Sequence Protein TABLE XII

HBV B27 Super Motif (No binding data available)

. TABLE XII

		НВV	Amino Acids	Frequency	(%)	
AYR	LKLIMPARF	107	6	15	75	1243
AYW	LRGLPVCAF	55	თ	19	95	1244
AYW	LRGTSFVVV	761	6	16	80	1245
AYW	LARFIIFLE	240	Ø	15	7.5	1246
AYW	PHCLAFSYM	531	O	19	95	1247
AYW	PHHTALROA	50	o	20	100	1248
AYW	PKVLHKRTL	06	თ	17	85	1249
AYR	OHFRILLL	9	Ø	15	7.5	1250
AYW	ORIVGILGF	623	G	18	06	1251
AYW	RKIPMGVGL	502	σ	16	80	1252
AYW	RKLPVNRPI	609	თ	16	80	1253
AYW	RKYTSFPWL	744	o	17	85	1254
AYW	RRAFPHCLA	527	o	19	95	1255
AYW	RRFIIFLFI	241	o	15	7.5	1256
AYR	RRLKLIMPA	105	o	15	75	1257
AYW	RRVAEDLNL	35	G	18	06	1258
AYW	SKICLGWLW	20	თ	17	85	1259
AYW	SRKYTSFPW	743	Ø	17	85	1260
AYW	TRHYLHILW	144	σ	20	100	1261
AYW	VHFASPLHV	819	σ	16	80	1262
AYW	VRFSWLSLL	331	đ	16	80	1263
AYW	VRRAFPHCL	526	თ	19	95	1264
AYW	YRPPNAPIL	132	თ	20	100	1265
AYW .	YRWMCLARF	. 532	თ	19	95	1266
AYW	AHLSLAGLPV	51	10	18	06	1267
AYW	AKSVOHLESL	546	10	17	85	1268
AYW	ARDVLCLRPV	12	10	15	7.5	1269
AYW	ARVTGGVFLV	356	10	18	06	1270
AYW	EHCSPHHTAL	46	10	20	100	1271
AYW	FRKIPMGVGL	501	10	16	80	1272
AYW	FRKLPVNRPI	608	10	16	80	1273
AYR	GRETVLENLV	140	10	15	75	1274
AYW	HHTALROAIL	51	10	19	95	1275
AYW	HKVGNFTGLY	54	10	19	95	1276
AYW	KRWGYSLNFM	576	10	17	85	1277
AYW	LHLYSHPIIL	490	10	16	80	1278
AYW	LHPAAMPHLL	428	10	20	100	1279
AYW	LHTLWKAGIL	148	10	20	100	1280
AYR	LKLIMPARFY	107	10	15	7.5	1281
AW	LARFIIFLFI	.240	10	15	7.5	1282
AYW	NKTKRWGYSL	573	10	15	7.5	1283
AYW	NRRVAEDLNL	34	10	17	85	1284
AYW	PHHTALROAI	50	10	20	100	1285
AYW	PHILVGSSGL	434	10	16	80	1286
AYW	QRIVGLGFA	623	10	18	06	1287
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TABLE XII		HBV B27 Super Mo	HBV B27 Super Motif (No binding data available)	ବ	. :	
Protein	Sequence	Position in HBV	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SeqID Num
AYW	RKYTSFPWLL	744	10	17	85	1289
AYW	RRAFPHCLAF	527	10	- 6	56	1290
AYW	RRFIIFLFIL	241	10	15	7.5	1291
AYW	SRKYTSFPWL	743	10	17	85	1292
AYW	SPLWDFSQF	375	10	. 19	9.6	1293
AYW	THKVGNFTGL	53	10	19	9.2	1294
AYW	TKRWGYSLNF	575	10	17	82	1295
AYW	TKYLPLDKGI	120	10	20	100	1296
AYW	TRILTIPOSL	186	10	. 91	80	1297
AYW	VHFASPLHVA	819	10	16	80	1298
AYW	VRFSWLSLLV	331	10	16	80	1299
AYW	VRRAFPHCLA	526	10	19	9.6	1300
AYW	WKVCORIVGL	619	10	17	82	1301
AYW	YRWMCLRRFI	235	10	19	95	1302
AYW	DHGAHLSLRGL	48	==	19	98	1303
AYW	IHLNPNKTKRW	568		5.	7.5	1304
AYW	IHTAELLAACF	714	=======================================	17	85	1305
AYW	LHPAAMPHLLV	428	=	17	85	1306
AYW	LHTLWKAGILY	148	==	20	100	1307
AYW	LROALCWGEL	55		18	06	1308
AYW	LARFIIFLFIL	240	-1	15	7.5	1309
AWW	PHHTALROAIL	50		19	9.2	1310
AW	PKFAVPNLOSL	394	=	19	95	1311
AYW	PKVLHKRTLGL	06 .		17	85	1312
AYW	PRTPARVTGGV	352	=	18	06	1313
AYW	GRIVGLLGFAA	623		18	06	1314
AYW	RKLPVNRPIDW	609		16	80	1315
AYW	RRFIIFLFILL	241	=	15	7.5	1316
AYR	RRLKLIMPARF	105	=	15	7.5	1317
AYW	SHPIILGFRKI	494	=	. 16	80	1318
AYW	SKLCLGWLWGM	20	=	17	85	1319
AYW	SRKYTSFPWLL	743	=	17	85	1320
AYW	THKVGNFTGLY	. 53		19	92	1321
AYW	TKRWGYSLNFM	575	=	17	85	1322
AYW	TRHYLHTLWKA	144	-	20	100	1323
AYW	VHFASPLHVAW	819		16	80	1324
AYW	VRRAFPHCLAF	526	=	19	92	1325
AYW	WKVCORIVGLL	619	-	17	85	1326
AYW	YRWMCLRRFII	235	11	19	92	1327

	SEQ ID NO:	1328	1329	1330	1331	1332	1333	1334	1335	1336	1337	1338	1000	1340	1342	1343	1344	1345	1346	1347	1348	1349	1350	1351	1352	1353	400	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365	1366	1367	1368	1369	1370	1371	1372	1373
	Conservancy (%)	85	85	100	06	80	80	92	06	100	95	on r	C - 6	n c	9 5	9 5	100	06	98	95	85	06	85	100	100	ອີດ	o u	. C	5 5	. so . so	06	100	95	80	100	100	95	80	06	95	06	7.5	85	80	7.5
	Sequence Frequency	17	17	20	18	16	16	-16	18	. 50	9 ,	6 +		- 4	9 5	o 6	20	18	19	19	1.7	18	17	20	50	5 0		B C	5 5	17	18	. 20	19	16	20	20	19	16	18	19	18	15	17	16	15
<u>r Motif</u>	No. of Amino Acids	80	80	80	80	œ	æ ·		&	œ (x 0 (x o o	.	ο α	• «	o 00	- ∞	- ∞	80	80	80	œ	60	ထ	∞ •	x 0 c	00	o «	• œ) co	80	60	80	80	œ		80	80	æ	80	80	80	89	∞ .	œ
HBV B58 Super Motif	Position	431	. 34	166	19	822	329	069	69	48	523	3/4	24-	821	- 30	63	333	536	635	518	545	735	715	52	149	515	04	4 - 5 2 - 5 2 - 5	55	742	408	412	108	103	136	430	641	-1	355	130	779	692	797	15	351
	Sequence	AAMPHLLV	ASALYREA	ASFCGSPY	ASKLCLGW	ASPLHVAW	ASVRFSWL	AIPIGWGL	CALRETSA	CSPHHTAL	CSVVHKAF	ENLVVUP FTM EM V	EABSBSGA	FASPI HVA	FSPTYKAF	FSSAGPCA	FSWLSLLV	FSYMDDVV	FTQCGYPA	FTSAICSV	GAKSVOHL	GTDNSWL	HTAELLAA	HTALROAI	HILWKAG	LAUFISA	105 JUST	I SI I VPFV	LSLRGLPV	LSRKYTSF	LSSNLSWL	LSWLSLDV	LTFGRETV	MSTTDLEA	NAPILSTL	PAAMPHLL	PALMPLYA	PARDVLCL	PARVTGGV	PAYRPPNA	PSRGRLGL	PTGWGLAI	PTTGRTSL	PTVOASKL	PTVWLSVI
Table XIII	Protein	Σ.	SP.	젍	Ą	ğ	2 3	₹:	×	2 8	₹ 8	¥	€ 5	<u> </u>	<u></u>	×	№	젒	젒	젒	젍	젍	점 :	3	₹ 8	₹ ‡	<u></u> } ⊊	₫ 2	š×	ಕ	ಜ	점	i MC	×	9	ਲੂ :	ප්	×	ಜೆ	N C	젍	젍	ğ	3	A B

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SEG ID NO.	1374	137	1376	1377	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387	1388	1389	1390	0061	1393	1394	1395	1396	1397	1398	1399	1400	140.5	1403	1404	1405	1406	1407	1408	1409	1410	1411	1412	1413	1414	1415	1416	1417	1418	
(%)	95	120	06	95	75	06	100	75	95	98	80	75	82	95	100	100	6 6	00.) (C)	96	85	06	80	80	56 6	95	95 79	် စ	95	95	95	06	95	06	98	95	92	95	100	85	96	06	95	
Frequency	19	24	18	19	15	18	20	15	. 61	19	16	. 5	17	19	50	50	- 6		17	19	17	18	16	16	<u>6</u>	9 0	07 -	9 9	19	19	19	18	19	-	19	19	. 61	19	20	17	19	18	19	
Amino Acids	8	80	හ	8	80	80	හ	ဆ	æ	80	80	æ ·	∞	∞ ⊤	.	യ ദ	co or	ο α	o &	o	6	6	o	6 0 (o	o	ით	ით	. 6	თ	O	თ	6	တ	o	6	O	6	o	o	o	6	თ	
	528	96	9.5	64	136	S	141	104	53	519	168	105	798	391	115	358	0 0	32	746	632	34	19	069	471	689	196	/1	821	366	658	63	536	656	59	635*	518	50	52.	149	547	574	534	45	
Padreike	RAFPHCLA	RTLGLSAM	SALYREAL	SSAGPCAL	SSGTVNPV	SSKPROGM	STLPETTV	STTDLEAY	TALROAIL	TSAICSVV	TSGFLGPL	TTDLEAYF	TIGRISLY	VSWPKFAV	MNANASA	VIGGVEV	DO COLON	>CWEN 5X	YTSFPWLL	AAPFTQCGY	ASALYREAL	ASKLCLGWL	ATPTGWGLA	CSANLYVSL	DAIPIGWGL	DSWWTSLNF	FANATPTGW	FASPLHVAW	FAVPNLOSL	FSPTYKAFL	FSSAGPCAL	FSYMDDVVL	FTFSPTYKA	FTGLYSSTV	FTGCGYPAL	FTSAICSVV	GAHLSLRGL	HTALROAIL	HTLWKAGIL	KSVOHLESL	KTKRWGYSL	LAFSYMDDV	LSFLPSDFF	
	æ	×	2	×	₩ A	8	NC C	×	3		<u>~</u>	×	ğ :	로 :	3 8	₹ 8	à 6	d 2	ಕ್ಷ ಕ್ಷ	હ	2	2	ದ್ದ	전 8	호 :	<u> </u>	<u> </u>	ಕ್ಷ ಕ್ಷ	ğ.	ರ	×	ೱ					×	2	젙	점	절	점	3	

Table XIII

HBV B58 Super Motif

	SEQ ID NO:	1420	1421	1422	1423	1424	1425	1426	142/	1428	1429	1431	1432	1433	1434	1435	1436	1437	1438	1439	1440	1442	1443	1444	1445	1446	1447	1448	1449	1450	1451	407	403	1455	1456	1457	1458	1459	1460	1461	1462	1463	1464	1465	
	Conservancy (%)	95	7.5	100	7.5	75	75	ာ မ	85 2.5	6.0) (4)	က Co	9 6 92	7.5	95	06	80	95	080	90	3 6	7.55	100	7.5	85	80	80	75	82	100	80 80 80	0 0	90	100	85	80	7.5	95	100	80	80	06	80	. 95	
	Sequence Frequency	19	15	20	15	15	15					~ ~	17	£.	19	18	16	- 19	16	 80 C	0.7	. t	20	15	17	16	16	15	17	20	<u> </u>	o (o 4		17	16	15	19	20	16	16	18	16	19	
er Motif	No. of Amino Acids	6	6	6	6	တာ (တေ	3 7 (on c	n o	n cr	ာတ	6	6	6	න ්	တေ	တ	ന ര	n c	n on	. 6	6	6	6	6	တ	6	တေ	5 7 (n c	n d	, <u>t</u>	9	10	10	10	10	10	10	10	10	10	
HBV B58 Super Motif	Position	510	349	140	16	က	137	404	56. 707	103	7.20	35.5 35.5 35.5	797	351	654	57	18	528	167	. 65	600	1 t C T	141	104	716	33	764	168	798	48	99	4 (20 m	360 166		329	069	61.	310	298	689	196	32	631	
	Sequence	LSPFLAOF	LSPTVWLSV	LSTLPETTV	LSVPNPLGF	LSYOHFRAL	LIFGHEIVL	LINILSSNL	METTOLEAN	MS11DLEAT	NSCANDING	PARVIGGVE	PTTGRTSLY	PTVWLSVIW	QAFTESPTY	OAILCWGEL	OASKLCLGW	RAFPHCLAF	RIGDPAPNM	SAGPCALRE	SAST CAST	SSSTVNPV	STLPETTW	STTDLEAYF	TAELLAACF	TASALYREA	TSFVYVPSA	TSGFLGPLL	TTGRTSLYA	VSIPWTHKV	WSPCACGIL	MODELLA MARKET	VSI NEMBOA	ASECGSPYSW	ASKICLGWLW	ASVRFSWLSL	ATPTGWGLAI	CAFSSAGPCA	CTCIPIPSSW	CTIPAGGTSM	DATPTGWGLA	DSWWTSLNFL	DTASALYREA	FAAPFTQCGY	
Table XIII	Protein	ಭ	AB M	ST.	№	ಕ :	3 8	걸	₫ >	< ∑	2 8	් ස		AB.	젗	22	3	g i	₹	× ¿	2 2	3 ≥	3	· ×	젃	ST.	젍	≈	점 :	ಕ :	≩ ∂	} 6 6	₫ & -	ද් ද	200	2	රු	×	8	Æ	젍	26	22	ಶ	

	SEQ ID NO:	1466	1467	1468	1469	1470	1471	1472	1473	1474	1475	1476	1477	1478	1479	1480	1481	1482	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	1493	1494	1495	1490	149R	1499	1500	1501	1502	1503	1504	1505	1506	1507	1508	1509	1510	1511
	Conservancy (%)	100	95	190	7.5	7.5	80	85	100	06	98	100	95	75	32	06	100	100	75	06	7.5	06	06	66	75	06	S 6	82	08	0¢1	08	081	00	9 6	06	95	06	85	95	80	7.5	. 80	7.5	95	7.5	85
	Sequence Frequency	20	19	38	15	15	16		20	18	19	20	19	. .	7.1	æ -	20	50	. 5	- 0	5	æ :	8	6	15	æ «	6 r	17	16	06	9-0	0 F			. 4	19	18	17	19	16	15	16	15	19	15	17
Motif	No. of Amino Acids	10	10	10	10	10	10	10	0	10	0 1	0 1	0 :	<u></u>	0 ;	0	2	10	<u></u>	10	10	9	2	0 :	9 ;	0.	0 ;	0 :	0 :	o ;	0 9	- -	2 5	2 5	10	10	10	10	10	10	0	10	10	10	10	=
HBV B58 Super Motif	Position	333	656	635	134	13	763	715	149	534	415	336	53	349	742	408	140	412	ന	189	103	775	131	641	145	355	130	797	15	351	179	/0	ζ <u>.</u> α	103	35.0 C.00 C.00	520	64	716	53	S. S	747	764	168	37	580	721
	Sequence	FSWLSLLVPF	FTFSPTYKAF	FTOCGYPALM	GSSSGTVNPV	GINLSVPNPL	GTSFVYVPSA	HTAELLAACF	HTLWKAGILY	LAFSYMDDVV	LSLDVSAAFY	LSLLVPFVQW	LSLAGLPVCA	LSP I VWLSVI	LSAKYISHPW	LSSNLSWLSL	LSTLPETTW	LSWLSLDVSA	LSYCHFIKLL	LTIPOSLDSW	MSTTDLEAYF	PADDPSRGRL	PAGGSSSGTV	PALMPLYACI	PAPCNFFTSA	· PARVIGGVFL	PAYHFRIAFI	PIIGHISLYA	FIVOASKICE	PIVWLSVIWM	CAGFFLL IRI	CALCWAGELM	OASKI CI GW	OSIDSWATS	RTPARVTGGV	SAICSVVRRA	SSAGPCALRF	TAELLAACFA	TALROAILCW	TASALYREAL	TSFPWLLGCA	TSFVYVPSAL	TSGFLGPLLV	VAEDLNLGNL	YSLNFMGYVI	AACFARSRSGA
Table XIII	Protein	W	ಜ	젍	8	8	젍	젍		ಶ :	전 :	3	× ;	£ 8	₹ 8	₹ :	2 5	전 1	z ;	2 2	×	덛 ?	3 (덛 :	× {	걸 :	3 8	₹ 5	3 2	<u> </u>	§ 2	3 6	: C		절	젍	×	ಜ	SH SH	2	젍	전	8	전	ಕ್ಷ	전

	SEQ ID NO:	1512	1513	1514	1515	1516	1517	1518	1519	1520	1521	1522	1523	1524	1525	1526	1527	1528	1529	1530	1531	1532	1533	1534	1535	1535	1537	2000	1539	7.7	1542	1543	1544	1545	1546	1547	1548	1549	1550	1551	1552	1553	1554	1555	1556	1557
	Conservancy (%)	95	80	95	130	100	100	7.5	80	95	95	06	100	06	95	. 06	. 982	80	82	95	06	82	06	95	100	ים מ	7.5	<u>د</u> د	95	2. 4.	06	06	80	7.5	06	98	140	95	80	7.5	06	95	06	95	95	100
	Sequence Frequency	19	16	19	26	20	50	15	16		19	18	20	18	19	18	17	16	17	19	18	17		19	20	D 1		<u> </u>	57 Y	. .	. 60	. 82	16	15	18	19	28	19	16		18	19	18	19	6- 6-	20
er Motif	No. of Amino Acids	11	=	=	=	=	11	=	=	.11	=	=	=======================================	=	=	Ξ	=	=	=	=	=	= :		= :	- ;	- 1	= ;	- ;	= :	= =	= =	Ξ	==	=	=		=	-11	11	=	****	11	=	-	= :	-
HBV BS8 Super Motif	Position	632	329	61	69	48	310	689	32	374	687	63	333	536	656	20	545	763	715	52	105	574	. 534	515	336	က္က	349	742	4 C	553	189	404	185	==	355	130	351	654	179	18	402	528	353	127	520	165
	Sequence	AAPFTOCGYPA	ASVRFSWLSLL	CAFSSAGPCAL	CALRFTSARRM	CSPHHTALROA	CTCIPIPSSWA	DATPTGWGLAI	DTASALYREAL	ESRLWDFSQF	FADATPTGWGL	FSSAGPCALRF	FSWLSLLVPFV	FSYMDDVVLGA	FTFSPTYKAFL	GAHLSLRGLPV	GAKSVOHLESL	GTSFVYVPSAL	HTAELLAACFA	HTALROAILCW	ISCLTFGRETV	KTKRWGYSLNF	LAFSYMDDVVL	LAGETSAICSV	LSILVPFVQWF	· LSLHGLPVCAF	LSPTVWLSVIW	LSHKYISHWL	LSWLSLDVSAA	TEGRETALEY	LTIPOSLDSWW	LTNLLSSNLSW	LTRILTIPOSL	PARDVLCLRPV	PARVTGGVFLV	PAYRPPNAPIL	PTVWLSVIWMM	QAFTFSPTYKA	QAGFFLLTRIL	QASKLCLGWLW	OSLTNLLSSNL	RAFPHCLAFSY	RTPARVTGGVF	RTPPAYRPPNA	SAICSVVRRAF	SASFCGSPYSW
Table XIII	Protein	ಹ	AG	×	×	3	₩	젍	2	ೱ		×	№	್ಷ	⊈	×	ජ	ಜೆ	ೱ	3	3	ದೆ :		점 :	₩ 3	× ;	₹	₫ 8	첫 8	3 <u>5</u>	} &	් ද	№	×	젒	3	%	젍	№	S)V	젒	ಶ	전	3	젍 :	

Table XIII		HBV B58	IBV B58 Super Motif		·	
Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
Σ.	SSNLSWLSLDV	409	11	18	06	1558
점	TSAICSVVRRA	519	11	19	95	1559
젒	TSFPWLLGCAA	747	11	15	75	1560
№	TSGFLGPLLM	168	=	15	7.5	1561
	VSWPKFAVPNL	391		19	95	1562
젙	WITHKVGNFTGL	52	=======================================	- 61	95	1563
2	YTSFPWII GCA	746	-		7.5	1564

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Table XIV

			Amino Acids	Frequency	(%)	
	ALCWGEL	58	8	18	06	1565
	APFTQCGY	633	80	19	95	1566
	AVPNLOSL	397.	83	19	95	1567
	CIPIPSSW	312	ဆ	20	100	1568
	CLGWLWGM	23	80	17	85	1569
	CLIFLEN	253	œ	. 20	100	1570
	CLRRFIIF	239	80	19	95	1571
	CORINGIL	622	ဆ	17	85	1572
	DIDPYKEF	31	80	18	06	1573
	DLLDTASA	59	80	17	85	1574
	DPRVRGLY	122	ဆ	16	80	1575
	DPYKEFGA	33	æ	18	06	1576
	DVLCLRPV	14	හ	19	95	1577
	E.GEERL	122	æ	16	80	1578
	ELLAACFA	718	80	18	06	1579
	FIIFLFIL	243	83	16	80	1580
	FILLCU	248	89	16	80	1581
	RGPLLVL	171	80	15	7.5	1582
	FLWLDY	256	89	19	95	1583
	FPWII GCA	749	8	15	7.5	1584
	FVGISPTV	346	80	- 10	56	1585
	FVOWFVG	342	80	6+	56	1586
	FVYVPSAL	992	8	18	06	1587
	GLSPFLIA	509	60	19	95	1588
•	GLSPTVML	348	89	20	100	1589
	GMLPVCPL	. 265	89	18	06	1590
	GPLLVLOA	173	80	19	95	1591
	GVGLSPFL	507	æ	16	80	1592
	HLYSHPII	491	æ	16	80	1593
	HPAAMPHL	429	æ	20	100	1594
	IIFLFILL	244	80	16	80	1595
	IILGFRKI	497	80	16	80	1596
	ILCWGELM	59	80	. 41	06	1597
	ILLCLIF	249	80	20	100	1598
	ILRGTSFV	760	80	16	80	1599
	LTIPOSL	188	60	19	92	1600
	IPIPSSWA	313	80	20	100	1601
	IPOSLDSW	191	80	18	06	1602
	IPSSWAFA	315	83	16	80	1603
	IVGLLGFA	625	8	18	06	1604
	KIPMGVGL	203	8	16	80	1605
	KICLGWIW	21	8	17	85	1606
	KLIMPARF	108	8	15	75	1607
	KLPVNBPI	610	8	16	80	1608
	KVGNFTG	55	8	19	95	1609
			•			
	KA IKBI		30	17	25.5	1610

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
ಕ	LIMPARFY	109	8	20	100	1612
ರ	LLAGFTSA	514	60	19	95	1613
≩	LICUFL	251	œ	20	100	1614
3	LLDTASAL	30	80	17	85	1615
≩	LLDYOGML	260	8	19	95	1616
ಕ	LLGCAANW	752	æ	16	. 80	1617
ಕ	LLGFAAPF	628	80	19	95	1618
₹	LLGWSPQA	63	80	17	85	1619
₹.	· LLCUFL	250	æ	20	100	1620
8	LPIFFCL	378	80	20	100	1621
ರ	LLSLGIML	563	80	19	9.2	1622
ರ	LLSSNLSW	407	ω	18	90	1623
≩	LLTRILTI	184	60	16	80	1624
ಕ	LLVGSSGL	436	80	16	80	1625
≥	LLVLOAGF	175	89	19	95	1626
≩	LLVPFVQW	338	80	20	100	1627
ಕ	LMPLYACI	643	80	19	95	1628
≥	LPIFFCLW	379	83	20	100	1629
ರ	LPIHTAEL	712	80	17	85	1630
≩	LOAGFFL	178	æ	19	98	1631
ಕ	LOSLTNIL	401	80	20	100	1632
≩	LVLOAGFF	176	80	19	98	1633
≩	LVPFVQWF	339	ထ	20	100	1634
3	LVSFGVWI	119	80	18	06	1635
ರ	· LWDFSQF	377	89	20	100	1636
ರ	MPLSYQHF		89	20	100	1637
8	MOLPHICAL	_	80	15	. 75	1638
≩	MOWNSTTF	109	æ	16	80	1639
ರ	NLNVSIPW	45	æ	19	92	1640
ರ	NEOSLTNE	400	ဆ	20	100	1641
≩	NLSVPNPL	15	æ	15	7.5	1642
ರ	NPNKTKRW	571	æ	15	7.5	1643
≥	PIFFCLWV	380	œ	20	100	1644
ರ	PIHTAELL	713	æ	17	85	1645
≩	PIPSSWAF	314	89	20	100	1646
≩	POSLDSWW	192	ω	18	06	1647
×	PVCAFSSA	29	ಹ	19	92	1648
ರ	PVNRPIDW	612	8	17	85	1649
×	CLDPARDV	œ	œ	16	80	1650
ರ	RIVGLLGF	624	ω	18	90	1651
ರ	RLKLIMPA	. 901	ω	15	7.5	1652
9	RPPNAPIL	133	æ	20	100	1653
9	ROLLWFHI	86	89	18	06	1654
ರ	RVAEDLNL	36	œ	19	98	1655
ರ	RVHFASPL	818	œ	16	80	1656
ಕ	RVTGGVFL	357	œ	20	100	1657
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HBV B62 Super Motif

Table XIV

Sequence Position No. of Modes Sequence Constituence SLDVSAMF 416 8 15 19 SLDVSAMF 416 8 15 19 SPADGIL 67 8 17 17 SPADGIL 8 17 17 17 SPADGIL 8 17 17 17 SPADGIL 8 17 17 17 SPADGIL 17 8 15 15 SPADGIL 17 8 16 15 VICHAGIL	Sequence Position No. ol Sequence Conservancy SLDVSAMF 511 8 19 55 SLDVSAMF 511 8 15 75 SLDVSAMF 511 8 15 75 SDCALON 511 8 15 75 SPOLLOG 511 8 15 75 SPOLLOG 659 8 17 85 SPOLLOG 172 85 17 85 SPOLLOG 172 8 16 85 SPOLLOG 172 8 17 85 SPOLLOG </th <th>Table XIV</th> <th></th> <th>ZOG AGII</th> <th>IIDA DOZ SUPEL MOIII</th> <th></th> <th></th> <th></th>	Table XIV		ZOG AGII	IIDA DOZ SUPEL MOIII			
SLDVSAAF 416 8 19 95 SPALACEL 67 81 19 75 SPALACEL 67 8 19 75 SPALACEL 87 8 19 75 SPALACEL 87 8 17 85 SPALACEL 86 8 17 85 SPALACEL 86 8 17 85 SPALACEL 86 8 17 85 SPALACEL 17 8 17 85 SOND-LEST 17 8 17 85 VALACEL 17 <th>SLDVSAAF 416 8 19 95 SPALACK 581 8 19 75 SPALACK 581 8 19 75 SPALACK 61 8 19 75 SPALACK 61 8 17 65 SPALACK 61 6 17 65 SPALACK 172 8 17 65 SPALACK 16 8 17 65 SPALACK 17 8 17 65 SPALACK 16 8 17 75 SPALACK 17 8 17 75 VALACK 17 8</th> <th>Protein</th> <th>Sequence</th> <th>Position</th> <th>No. of Amino Acids</th> <th>Sequence Frequency</th> <th>Conservancy (%)</th> <th>SEQ ID NO:</th>	SLDVSAAF 416 8 19 95 SPALACK 581 8 19 75 SPALACK 581 8 19 75 SPALACK 61 8 19 75 SPALACK 61 8 17 65 SPALACK 61 6 17 65 SPALACK 172 8 17 65 SPALACK 16 8 17 65 SPALACK 17 8 17 65 SPALACK 16 8 17 75 SPALACK 17 8 17 75 VALACK 17 8	Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
SPOLOGIA 581 8 15 75 SPOLOGIA 511 8 19 95 SPOLOGIA 67 511 8 19 95 SPOLOGIA 888 8 17 76 SPOLOGIA 10 8 17 76 SPOLOGIA 10 8 17 76 SPOLOGIA 10 8 17 76 SPOLOGIA 112 8 17 76 SPOLOGIA 113 8 17 76 SPOLOGIA 114 7 8 17 76 SPOLOGIA 115 8 17 76 SPOLOGIA 116 8 17 76 SPOLOGI	SPILAGE 581 8 15 75 SPILAGE 571 8 19 95 SPOLOGIE 67 8 17 85 SPOLOGIE 67 8 17 85 SPOLOGIE 67 8 17 85 SPOLOGIE 73 8 17 85 SPOLOGIE 73 8 17 85 SPOLOGIE 73 8 17 85 SPOLOGIES 73 8 17 85 SPOLOGIE 73 8 17 85 SOVASSICA 142 8 16 85 TOCOPPAL 57 8 16 85 TOCOSPAL 636 8 17 85 TOCOSPAL 636 8 16 85 TOCOSPAL 177 8 16 85 VOLOGIE 177 8 16 86 VOLOGIE 177	25	SLDVSAAF	416	8	19	95	1659
SPOLOCAL 511 8 95 SPOLOCAL 617 86 95 SPOLOCAL 617 86 95 SPOLOCAL 630 8 17 85 SPOLOCAL 630 8 17 85 SPANDALGA 631 8 17 85 SWALES 739 8 17 85 SWALES 57 8 17 85 SWALES 57 8 17 85 SWALES 57 8 17 85 SWALES 691 8 17 85 SWALES 691 8 17 85 INWEGRAL 150 8 16 95 INMEGRAL 177 8 17 85 INMEGRAL 177 8 18 95 WINDOCAM 177 8 18 95 WINDOCAM 177 8 18 95	SPINAGE 511 8 SPOACCIL 671 8 SPOACCIL 675 8 STOACCIL 675 8 STOACCIL 17 85 STOACCIL 17 85 SWARK 739 8 17 85 SWARK 150 8 17 85 INVESTAL 681 8 17 85 INVESTAL 150 8 16 95 VALDYCAN 177 8 17 85 VALDYCAN 177 8 16 95 VALDYCAN 177 8 17 17 VALDYCAN 177 8 16 95 VALDYCAN 177 8 16 95 VALDYCAN 172	ಶ	SLNFMGYV	581	88	15	7.5	1660
SPORCAL 67 8 SPORCAL 67 8 17 85 SPORTAGE 350 8 17 85 SPORTAGE 536 8 17 85 SPORTAGE 536 8 15 75 SPORTAGE 548 8 15 75 SWALSHY 142 8 15 75 ILMAGIL 57 8 16 100 ILMAGIL 57 8 16 95 ILMAGIL 60 8 17 8 75 ILMAGIL 57 8 16 95 ILMAGIL 32 8 16 95 ILMAGIL 32 8 16 95 VICAKSON 412 8	SPONGCIL 67 8 SPONGCIL 67 8 SPONGCIL 67 8 SPONGCIL 68 8 17 85 SPONGCIL 17 85 75 75 STYMASH 17 85 75 75 SONLSRY 142 8 15 75 SONLSRY 142 8 15 75 ILMMAGIL 150 8 16 95 TIMMAGIL 60 8 17 40 TIMMAGIL 60 8 17 40 TIMMAGIL 60 8 16 95 MULDOGRAM 100 8 16 95 VALLANCARRIL 17 8 16 95 VALLANCARRIL <td>ದ್ದ</td> <td>SPFLLAOF</td> <td>511</td> <td>ω</td> <td>19</td> <td>95</td> <td>1661</td>	ದ್ದ	SPFLLAOF	511	ω	19	95	1661
SPSY/PSHL 808 85 SPSY/AGEL 659 8 17 75 SVPTAKAR 350 8 17 75 SVPTAKAR 17 8 17 75 SVPARAT 733 8 17 75 SVPARAT 733 8 17 8 SVPARAT 150 8 16 16 95 TPHGALL 57 8 17 8 17 8 16 100 TPHGALL 57 8 16 8 16 8 16 100 TPHGALL 57 8 17 8 17 8 16 8 16 <td>STEATING 808 8 17 85 STYCAFI 699 8 15 75 SPITYALE 150 8 15 75 SPITYALE 150 8 17 85 SPITYALE 150 8 17 85 SWASHAC 773 8 17 85 SWASHAC 150 8 17 85 SWASHAC 150 8 17 85 TITATION 142 8 17 85 TITATION 8 17 85 75 TITATION 8 17 85 75 MUDICATA 691 8 16 95 VINDAGAN 177 8 17 85 VINDAGAN 177 8 16 95 VINDAGAN 177 8 16 95 VINDAGAN 177 8 16 95 VINDAGAN 174</td> <td>~</td> <td>SPOAGGIL</td> <td>67</td> <td>æ</td> <td>17</td> <td>85</td> <td>1662</td>	STEATING 808 8 17 85 STYCAFI 699 8 15 75 SPITYALE 150 8 15 75 SPITYALE 150 8 17 85 SPITYALE 150 8 17 85 SWASHAC 773 8 17 85 SWASHAC 150 8 17 85 SWASHAC 150 8 17 85 TITATION 142 8 17 85 TITATION 8 17 85 75 TITATION 8 17 85 75 MUDICATA 691 8 16 95 VINDAGAN 177 8 17 85 VINDAGAN 177 8 16 95 VINDAGAN 177 8 16 95 VINDAGAN 177 8 16 95 VINDAGAN 174	~	SPOAGGIL	67	æ	17	85	1662
SPTWALEY SPTWALEY SPRINGLE SWENEGE 17 SWENEG	SPYWALSY 530 8 15 75 55 75 55 75 55 75 57 55 75 57 57 57	2 :	SPSVPSHL	808	Φ (17	82	1663
SYMPLIGHT SYMPLIGH SY	SYMPLICATE	26	SPTVMLSV	350	Φ,	15	7.5	1664
SOPHINGE 17 8 17 75 SWIPHIGE 17 8 15 75 WALSHOY 739 8 16 90 TURKER 150 8 16 90 TURKER 691 8 17 85 TOCOSYPAL 636 8 16 80 TWANSWAR 352 8 17 85 TWANSWAR 352 8 17 85 TWANSWAR 352 8 15 95 VADAGAR 352 8 18 95 VADAGAR 352 8 18 95 WALDONG 354 8 18 95 WALDONG 352 8 18 95 WALDONG 354	Sychelight 17 8 175 Sychel	ಶ :	SPTYKAFL	628	∞ ·	19	9.2	1665
SVOLESK 548 8 17 85 SVOLESK 548 8 17 95 TLPETYV 142 8 16 100 TIPPIGMEL 57 8 16 100 TIPPIGMEL 57 8 16 100 TOCGYPAL 636 8 16 8 15 TOCGYPAL 636 8 17 8 17 8 TOCGYPAL 100 8 17 8 15 8 15 10 10 10	SVOHERA 548 8 17 85 SVOHERA 548 8 17 95 InPETIVA 142 8 16 10 TIPPIGALI 57 8 16 10 TIPPIGALI 636 8 16 16 16 TIPPIGALI 636 8 16	8 6	SVPNPLGF	17	σ	15	7.5	1666
The Permitted	NAMERINA 1439 8 10 100 100 100 100 100 100 100 100 10	전 :	SVOHLESL	548	00	17	85	1667
TUMKAGIL 142 8 20 100	TUMKAGIL 142 8 20 100	ಶ :	SWLSRKY	739	20	18	06	1668
TPMAGIL 150 8 100 TPMAGIL 150 8 100 TPMAGIL 150 8 100 TPMAGIL 150 8 100 TPMAGIL 100 8 10 10 10 10 10 10 10 10 10 10 10 10 10	Thy Middle 150 8 100 Thy Middle 150 8 100 Thy Middle 150 8 150 100 Thy Middle 150 8 15 15 150 Thy Middle 150 8 15 15 150 Thy Middle 175 15 150 Thy Middle 175 150 Thy	2	TLPETTW	142	∞	20	100	1669
TPHGGLL 57 8 15 75 TYCHONGLA 691 8 16 85 TYCKOSTPAL 636 8 16 85 TVMLSWIM 259 8 15 75 VLDYGGR 177 8 19 95 VLDYGGR 177 8 19 95 VLDYGGR 177 8 18 96 VPADAGFL 177 8 18 96 VPADAGFL 177 8 18 96 VVGAKSV 369 8 18 90 VNLRASUNS 414 8 8 10 90 WISTINF 335 8 16 90 90 WALDINGI 125 8 16 90 90 VLHLIMA 147 8 19 95 MALLING 147 8 19 95 ALMANICA 640 8 18 90	TypeKGML	ಶ	TLWKAGIL	150	∞	20	100	1670
TPTGWGLA 691 B 16 B0 TOCKWALL 635 B 16 B0 TWEGRAL 100 B 17 B5 TWUNCKIN 252 B 19 95 VLOAGFRAL 340 B 19 95 VFALLOWICK 340 B 19 95 VFALLOWICK 17 B 16 90 VICAKSY 542 B B B B WILLDING 17 B 16 90 WILLDING 17 B B B B WILLDING 125 B B B B WILLDING 125 B B B B WILLDING 125 B B B B WILLIAM 127 B B B B WILLIAM 127 B B B B WILLIAM 128 <td>TPTGWGLA 691 B 16 B0 TOCKPALL 635 B 16 B0 TWNENGRAL 100 B 17 B5 TWNENGRAL 100 B 17 B5 VLOAGER 177 B 17 B VLOAGER 340 B 19 95 VPACOMEN 340 B 19 95 VPACOMEN 340 B 19 95 VPACOMEN 340 B 18 90 VPACOMEN 340 B 18 90 VOASALCL 17 B 18 90 VOASALCL 17 B 18 90 WINCLEST 15 B 18 90 WINCLEST 125 B 19 90 WINCLEST 141 B 10 90 VILLIAM 141 B 10 90 VILLIAM 14<</td> <td>&</td> <td>TPPHGGLL</td> <td>57</td> <td>æ</td> <td>15</td> <td>7.5</td> <td>1671</td>	TPTGWGLA 691 B 16 B0 TOCKPALL 635 B 16 B0 TWNENGRAL 100 B 17 B5 TWNENGRAL 100 B 17 B5 VLOAGER 177 B 17 B VLOAGER 340 B 19 95 VPACOMEN 340 B 19 95 VPACOMEN 340 B 19 95 VPACOMEN 340 B 18 90 VPACOMEN 340 B 18 90 VOASALCL 17 B 18 90 VOASALCL 17 B 18 90 WINCLEST 15 B 18 90 WINCLEST 125 B 19 90 WINCLEST 141 B 10 90 VILLIAM 141 B 10 90 VILLIAM 14<	&	TPPHGGLL	57	æ	15	7.5	1671
TOCGYPAL 636 B 11 95 TOCGYPAL 636 B 17 85 TVMEXGRA 352 B 15 75 VLDVGGFL 177 B 19 95 VLDVGGFL 177 B 19 95 VPSALNA 340 B 18 90 VPSALNA 769 B 18 90 VOLASIC 17 B 16 80 VALLINGS 125 B 16 80 WILLGITSF 759 B 16 80 WILLGITSF 759 B 16 80 WILLGITSF 759 B 16 90 WILLGITSF 759 B 16 90 WILLDING 122 B 100 90 WILLDING 122 B 100 90 WILLDING 54 B 19 90 WILLDING	TOCGYPAL G36 B 17 F5	젍	TPTGWGLA	691	œ	16	80	1672
TWABGREL 100 8 17 85 VLDMGFAL 252 8 15 75 VLDMGFAL 177 8 19 95 VLDMGFAL 177 8 19 95 VPSALMEY 340 8 19 95 VPSALMEY 76 8 16 80 VMLGAKSV 542 8 18 90 WILLSTS 75 8 16 80 WILLSTS 75 8 16 80 WILLSTS 75 8 10 90 WILLSTS 75 8 10 90 WILLSTS 147 8 20 100 WILLSTS 147 8 20 100 WILLSTS 147 8 20 100 VLATUWAL 147 8 18 9 VLATUWAL 5 9 18 9 ALLWINGELM 58	TWARGRAL 100 8 17 85 TWARGRAL 100 8 17 8 75 VLONGER 259 8 19 95 VLOAGRAL 340 8 19 95 VPALINA 769 8 18 95 VPALINA 769 8 16 80 WILGISE 759 8 16 80 WILGISE 759 8 16 80 WILGISE 125 8 16 80 WILLIAMA 14 8 10 100 WILLIAMA 118 8 10 100 WILLIAMA 118 8 10 100 VLHTIAMA 51 8 16 9 VLHTIAMA 118 8 10 10 VLHTIAMA 51 8 10 10 VLHTIAMAL 52 8 18 9 VLHTIAMA <td>ಕ</td> <td>TOCGYPAL</td> <td>636</td> <td>80</td> <td>19</td> <td>95</td> <td>1673</td>	ಕ	TOCGYPAL	636	80	19	95	1673
TWM_SNW 352 8 15 75 VLDYCGM 259 8 19 95 VLDAGFR 177 8 19 95 VDASALINPA 340 8 16 95 VOASALINPA 17 8 16 80 VOASALINPA 125 8 16 80 WISLINZA 125 8 16 80 WASLINPA 125 8 10 90 WASLINPA 122 8 10 90 WASLINPA 122 8 10 90 WASLINPA 122 8 20 100 WASTINDKGI 122 8 20 100 WASTINDKGI 122 8 20 100 WASTINDKGI 122 8 18 9 WASTINDKGI 118 8 18 9 VOHERRAL 5 8 18 9 ALICWGELM	TWMLSNW 352 8 15 75 VLDYGGM 259 8 19 95 VLDAGFPL 177 8 19 95 VLDAGFPL 178 8 19 95 VPSALINA 789 8 18 95 VDASSIGL 17 8 18 90 VDASSIGL 17 8 18 90 VDASSIGL 175 8 16 80 WILGAKSV 125 8 16 80 WILLSTIPSA 1414 8 20 100 WILLSTIPSA 147 8 20 100 WILLSTIPSA 147 8 20 100 VLHTLWA 147 8 20 100 VLYPLOKGI 122 8 19 9 VLYPLOK 148 8 19 9 ALCSVVRAA 54 9 18 9 ALINELYACI	ಕ	TVNEKRRL	100	80	17	85	1674
VLDVQGM 259 B 19 95 VPCAGFR 177 B 19 95 VPSALNPA 769 B 18 90 VPSALNPA 769 B 16 90 VMLGAKSV 542 B 16 90 VMLGAKSV 542 B 16 80 WMLGAKSV 543 B 16 80 WMSLUVSA 414 B 20 100 WMSLLVSA 147 B 20 100 WMSLLVSA 147 B 20 100 VLHTAWA 147 B 20 100 VLHALMA 16 B 19 95 VLYSFGW 118 B 18 90 VCM-FRALL 5 B 19 95 ALCSVARBA 54 B 19 95 ALCOWEELM 54 B 19 95 ALCOWEELM <td< td=""><td>VLDYOGN 259 B 19 95 VLDYOGN 177 B 19 95 VPSALNPA 769 B 19 95 VPSALNPA 769 B 18 90 VULGASSACCL 17 B 16 80 VULGASSACCL 17 B 16 80 VULGASSACCL 759 B 16 80 WILGASSACCL 759 B 16 80 WILGASSACCL 17 B 16 80 WILGASSACCL 175 B 16 80 WILGASSACCL 175 B 16 80 WILGASSACCL 125 B 16 80 WILGASSACCL 147 B 20 100 WILGASSACCL 147 B 20 100 VLHILWIA 58 B 18 90 ALICANCELM 58 9 18 90</td><td>86</td><td>TVWLSVIW</td><td>352</td><td>60</td><td>15</td><td>7.5</td><td>1675</td></td<>	VLDYOGN 259 B 19 95 VLDYOGN 177 B 19 95 VPSALNPA 769 B 19 95 VPSALNPA 769 B 18 90 VULGASSACCL 17 B 16 80 VULGASSACCL 17 B 16 80 VULGASSACCL 759 B 16 80 WILGASSACCL 759 B 16 80 WILGASSACCL 17 B 16 80 WILGASSACCL 175 B 16 80 WILGASSACCL 175 B 16 80 WILGASSACCL 125 B 16 80 WILGASSACCL 147 B 20 100 WILGASSACCL 147 B 20 100 VLHILWIA 58 B 18 90 ALICANCELM 58 9 18 90	8 6	TVWLSVIW	352	60	15	7.5	1675
WOAGFPL 177 8 19 95 VPCAMINA 769 8 19 95 VPSALUNA 769 8 16 90 VOASKICL 17 8 16 80 VUCAKSY 542 8 16 80 WILGAKSY 759 8 16 80 WILGAKSY 125 8 16 80 WILGAKSY 125 8 16 80 WILLINGA 144 8 20 100 WILLINKA 147 8 20 100 VLHTLWKA 147 8 20 100 VLHTLWKA 147 8 20 100 VLHTLWKA 148 8 10 9 VLHTLWKA 118 8 10 9 VLHTLWKA 118 8 10 9 VLHTLWKA 5 8 18 10 VOEVKRAM 5	VPACAFR 177 8 19 95 VPACARPY 340 8 19 95 VPACARIC 17 8 16 90 VDASALOR 17 8 16 80 WILDAGASY 542 8 16 80 WILLAGASY 125 8 16 80 WILLAGASY 125 8 16 80 WILLAGASY 125 8 16 80 WILLAGALOR 335 8 20 100 WACLINGA 124 8 20 100 WACLINGA 122 8 20 100 WACLARIC 5 8 16 90 VLHTUWKA 118 8 16 90 VLHTUWKA 118 8 16 90 VLHTUWKA 52 8 16 90 VLHTUWKA 54 9 18 15 ALCAGARICA	8	VLDYGGM	259	60	19	95	1676
VPFNOWNY 340 8 19 95 VPSALNPA 769 8 18 96 VOASACL 17 8 18 90 VOLGAKSY 542 8 16 80 WLSLDYS 542 8 16 80 WILSLOYSA 414 8 20 100 WASLDYSA 147 8 20 100 WASLDYSA 147 8 20 100 WASLDYSA 147 8 20 100 WASLDYSA 118 8 19 100 YOHTMUL 5 8 19 15 75 ALICAMBLY MCI 642 9 16 95 ALICAMBLY 54 9 16 95	VPSALNA 340 B 19 95 VPSALNA 179 B 18 95 VOASKICL 179 B 18 90 VUCAKSY 542 B 16 80 WILSTOYR 759 B 16 80 WILSTOYR 125 B 19 95 WILSTOYR 147 B 20 100 WASLOYR 147 B 20 100 WALTIONER 147 B 20 100 WALTIONER 147 B 20 100 VIPLIDIGI 122 B 19 95 VIPLIDIGI 122 B 10 90 VOHERAL 5 B 19 95 ALLONGEM 54 9 18 95 ALLONGEM 54 9 18 95 ALLONGEM 54 9 16 95 ALONGWINSTF	~	NLOAGFFL	177	æ	19	95	1677
VPSALNPA 769 8 16 90 VOGAKUCL 17 8 16 90 VALGAKSY 542 8 16 90 VALGAKSY 759 8 16 80 WINTERSY 125 8 19 95 WINTERSY 125 8 20 100 WACLARFI 147 8 20 100 VALHILWAA 118 8 10 95 VALMPLY 640 8 18 90 VALMPLY 640 8 18 90 VASCWRRA 521 9 18 90 ALMPLYACI 642 9 18 95 ALMPLYACI 642 9 16 80 AMSTOLEA 102 9 16 80 AMSTOLEA 146 9 16 80 AMSTOLEA 146 9 16 100 CHFILLIVIL	VPSALNRA 769 8 18 90 VOASACLC 17 8 18 90 VACAKSY 542 8 16 80 WILLYPE 759 8 16 80 WILLYPE 125 8 20 100 WILLYDAGA 112 8 20 100 VALDAGI 122 8 20 100 VALDAGI 122 8 20 100 VALCADARI 118 8 20 100 VALCACIARIL 5 8 20 100 VALCANDELM 5 8 18 90 VALCACIAL 5 8 18 90 ALICAVARIA 5 9 19 95 ALOVACELM 54 9 19 95 ALOVACIA 54 9 19 95 ALOVACIA 54 9 19 16 AMONINSTF	~	VPFVQWFV	340	æ	19	95	1678
WOASKICL 17 8 16 80 WILGAKSV 542 8 18 90 WILGAKSV 542 8 18 90 WILGAKSY 759 8 16 80 WILGAKSY 125 8 20 100 WASLUPF 335 8 20 100 WASLUPF 335 8 20 100 WASLUPF 122 8 20 100 WASLUPF 147 8 20 100 WASLUPF 147 8 20 100 YALLOKGI 118 8 10 100 YALLOKGI 118 8 10 100 YALLOKGI 58 9 18 15 75 ALCOWERM 58 9 19 19 95 ALCOWERM 54 9 19 16 90 ALCOWERM 54 9 16 90 </td <td>VOASIGOL 17 8 16 80 VALGAKSY 542 8 16 80 WINTEPAY 759 8 16 80 WINTEPAY 125 8 19 95 WILLYPE 335 8 20 100 WACLARFI 237 8 20 100 WACLARFI 122 8 20 100 WALLAPKI 122 8 20 100 YOHTINKA 118 8 10 90 YOHTINKA 118 8 10 90 YOHTINKA 5 8 10 90 YOHTINKA 5 8 10 90 YOHTINKA 54 9 11 90 ALLMPLYKI 54 9 11 90 ALLMPLYKI 54 9 11 90 ALROWERTS 106 9 15 75 ALROWERTS <t< td=""><td>ರ್ಷ</td><td>VPSALNPA</td><td>169</td><td>æ</td><td>18</td><td>06</td><td>1679</td></t<></td>	VOASIGOL 17 8 16 80 VALGAKSY 542 8 16 80 WINTEPAY 759 8 16 80 WINTEPAY 125 8 19 95 WILLYPE 335 8 20 100 WACLARFI 237 8 20 100 WACLARFI 122 8 20 100 WALLAPKI 122 8 20 100 YOHTINKA 118 8 10 90 YOHTINKA 118 8 10 90 YOHTINKA 5 8 10 90 YOHTINKA 5 8 10 90 YOHTINKA 54 9 11 90 ALLMPLYKI 54 9 11 90 ALLMPLYKI 54 9 11 90 ALROWERTS 106 9 15 75 ALROWERTS <t< td=""><td>ರ್ಷ</td><td>VPSALNPA</td><td>169</td><td>æ</td><td>18</td><td>06</td><td>1679</td></t<>	ರ್ಷ	VPSALNPA	169	æ	18	06	1679
WULGAKSV 542 B 18 90 WULGAKSV 759 B 16 90 WILGAKSV 125 B 16 80 WILSLDYSA 414 B 19 95 WILSLDYSA 414 B 20 100 WALSLDYSA 414 B 20 100 WALSLDYSA 414 B 20 100 WALSLDYSA 418 B 20 100 WALSLDYSA 118 B 20 100 YLHTUWG 118 B 100 100 YLHTUWG 118 B 100 100 YLHTUWG 146 9 118 9 ALCSHAMAC 58 9 118 9 ALCSHAMAC </td <td>WLGAKSV 542 B 118 90 WILGAKSV 759 B 16 90 WILGAKSY 759 B 16 90 WILGAKSY 125 B 16 90 WILGARD 237 B 20 100 WILGALDKA 147 B 20 100 YLPLOKGI 122 B 20 100 YLPLOKGI 123 B 20 100 YLPLOKGI 124 B 20 100 YLPLOKGI 118 B 118 90 YLPLOKGI 640 B 120 100 YLPLOKGI 51 B 13 90 ALCSVEW 52 B 13 90 ALCSVERM 53 B 13 90 ALLONGELM 54 I 9 14 90 ALLONGELM 54 I 9 14 90</td> <td>3</td> <td>VOASKLCL</td> <td>17</td> <td>80</td> <td>16</td> <td>80</td> <td>1680</td>	WLGAKSV 542 B 118 90 WILGAKSV 759 B 16 90 WILGAKSY 759 B 16 90 WILGAKSY 125 B 16 90 WILGARD 237 B 20 100 WILGALDKA 147 B 20 100 YLPLOKGI 122 B 20 100 YLPLOKGI 123 B 20 100 YLPLOKGI 124 B 20 100 YLPLOKGI 118 B 118 90 YLPLOKGI 640 B 120 100 YLPLOKGI 51 B 13 90 ALCSVEW 52 B 13 90 ALCSVERM 53 B 13 90 ALLONGELM 54 I 9 14 90 ALLONGELM 54 I 9 14 90	3	VOASKLCL	17	80	16	80	1680
WILRGTSF 759 8 16 80 WILRGTSF 759 8 16 80 WILSLUVSA 114 8 20 100 WILSLUVSA 335 8 20 100 WILSLUVSE 335 8 20 100 WILSLUVSE 147 8 20 100 VILLILWKA 147 8 20 100 VILLILWKA 118 8 20 100 VOHERALL 5 8 18 95 ACHONEGLM 640 8 18 95 ALIMPLYACI 642 9 18 95 ALIMPLYACI 642 9 19 95 ALIMPLYACI 642 9 19 95 ALMONISTIF 108 9 16 95 AMOWINSTIF 108 9 16 9 AMOWINSTIF 102 9 16 9 AM	WILAGTSF 759 8 16 80 WILAGTSF 125 8 19 95 WASLUNFA 414 8 20 100 WASLUNF 335 8 20 100 WASLUNF 147 8 20 100 WASLUNF 147 8 20 100 YPALME 112 8 20 100 YPALMELY 640 8 18 90 YOHERQL 5 8 19 95 ALCSVERW 118 8 19 95 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 18 90 ALMOMISTIF 108 9 16 8 AMOWISTIF 108 9 16 8 AMOWISTIC 253 9 15 75 AMOWISTIC 253 9 16 9 CHELIVIL	ದ್ದ	WLGAKSV	542	80	18	06	1681
WIRTPPAY 125 8 19 95 WISLDVSA 414 8 20 100 WISLLVPF 237 8 20 100 WASLLVPF 237 8 19 95 WLLLWKG 147 8 20 100 YLHTUWK 118 8 18 90 YLHTUWK 640 8 20 100 YLHTUWK 118 8 18 90 YLHTUWK 640 8 18 90 YLLLWKGIM 521 9 18 90 ALCWSCWIM 54 9 18 90 ALLWOWERIA 54 9 18 90 ALLOWGELW	WIRTPPAY 125 8 19 95 WISLDVSA 414 8 20 100 WISLLOYSA 414 8 20 100 WISLLOYPE 237 8 20 100 WINCLARFI 237 8 20 100 VLHTLWKG 122 8 20 100 VLHTLWKG 640 8 20 100 VLYSFGW 640 8 19 95 VCHTRALL 5 8 19 95 ACLENKILL 5 8 19 95 ALLOYGELM 54 9 19 95 ALROYNER 54 9 19 95 ALROALCW 54 9 16 95 ALTOALLCW 54 9 16 95 ALTOALLCW 54 9 16 95 ALTOALLCW 54 9 16 9 AMOWNSTTF	ಕ್ಷ	WILRGTSF	759	80	16	80	1682
WLSLDVSA 414 8 20 100 WASLLVPF 335 8 20 100 WASLLVPF 335 8 20 100 WASLLVPF 147 8 20 100 VALLYBEGW 118 8 10 100 VALLARPLY 640 8 19 95 VOHERRIAL 5 8 19 95 ALCWGELM 58 9 19 95 ALCWGELM 54 9 19 19 95 ALCWGELW 54 9 19 16 95 ALCWGELW 102 9 16 9 16 9 ALCWGELW 102 9 15 <td>WLSLDVSA 414 8 20 100 WLSLLVPF 335 8 20 100 WLSLLVPF 335 8 20 100 WLSLLVPF 127 8 20 100 YLLDKGI 122 8 20 100 YLLDKGI 118 8 18 90 YPALMPLY 640 8 19 95 YPALMPLY 54 9 19 95 ACKPERALL 58 9 19 95 ALMPLYACI 642 9 19 16 95 ALMPLYACI 108 9 16 95 16 95 AMONINSTIF 108 9 16 9 15 75 ALMPLYACI 253</td> <td>3</td> <td>· WIRTPPAY</td> <td>125</td> <td>60</td> <td>19</td> <td>95</td> <td>1683</td>	WLSLDVSA 414 8 20 100 WLSLLVPF 335 8 20 100 WLSLLVPF 335 8 20 100 WLSLLVPF 127 8 20 100 YLLDKGI 122 8 20 100 YLLDKGI 118 8 18 90 YPALMPLY 640 8 19 95 YPALMPLY 54 9 19 95 ACKPERALL 58 9 19 95 ALMPLYACI 642 9 19 16 95 ALMPLYACI 108 9 16 95 16 95 AMONINSTIF 108 9 16 9 15 75 ALMPLYACI 253	3	· WIRTPPAY	125	60	19	95	1683
WLSLLVPF 335 8 20 100 WMCGRFI 237 8 19 95 VLHTUWKA 147 8 20 100 YLHTUWKA 147 8 20 100 YLHTUWKA 118 8 10 100 YLHTUWKA 640 8 18 90 YPALMPLY 640 8 18 90 YPALMPLY 640 8 18 90 AICSVNRAL 521 9 19 95 ALMPLYACI 642 9 18 95 ALMPLYACI 642 9 18 95 ALMPLYACI 642 9 16 95 ALMOWINSTITY 108 9 16 95 AMCOWINSTITY 253 9 16 9 AMCOWINSTITY 253 9 16 9 CIFILLYIL 253 9 16 9 CIPITY	WLSILVPF 335 8 20 100 WMCJRRFI 237 8 20 100 VLHTWKA 147 8 20 100 YLHTWKA 122 8 20 100 YLHTWKA 118 8 20 100 YVALMPLY 640 8 18 90 YPALMPLY 640 8 18 90 ALCSVYBRA 521 9 19 95 ALCSVYBRA 54 9 18 95 ALCSVYBRA 54 9 18 95 ALCSVYBRA 54 9 19 95 ALCSVYBRA 54 9 16 95 ALCSVYBRA 16 9 16 95 ALCSVYBRA	ಕ	WLSLDVSA	414	80	20	100	1684
WMCJARFI 237 8 19 95 YLHTLWKA 147 8 20 100 YLHTLWKA 122 8 20 100 YLLDKGI 122 8 18 90 YPALLMLY 640 8 19 95 YOHTRAL 521 9 19 95 ALCSVVRRA 58 9 18 90 ALLOWGELM 58 9 18 90 ALLWPLYACI 642 9 18 95 ALLOWGELM 54 9 19 95 ALLOWGELM 54 9 19 15 75 ALLOWGELM 54 9 16 95 16 95 ALLOWGELM 54 9 16 9 15 75 ALLOWGELM 54 9 16 9 16 9 AMSTOLLS 146 9 15 100 100	WMCLRFI 237 8 19 95 YLHTUWKA 147 8 20 100 YLHTUWKA 122 8 20 100 YLPDKGI 122 8 20 100 YLPDKGI 118 8 18 90 YPALMPLY 640 8 18 95 YOH-FRALL 5 8 19 95 ALCWGELM 58 9 18 90 ALMPLYACI 642 9 18 95 ALMPLYACI 642 9 18 95 ALMPLYACI 642 9 18 95 ALMPLYACI 642 9 16 95 ALMPLYACI 642 9 16 95 ALMPLYACI 168 9 16 95 AMAGNINSTIF 108 9 16 100 CUFLIVIL 253 9 16 9 CLIFLIVIL	SS	WLSLLVPF	335	80	20	100	1685
YLHTLWKA 147 B 20 100 YLPLDKGI 122 B 20 100 YLVSFGWW 118 B 18 90 YPALMPLY 640 B 19 95 YOHFRAL 5 B 19 95 ALCSVARA 58 9 19 95 ALMPLYACI 642 9 18 95 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 19 95 ALMOMINSTIF 108 9 16 80 AMOWINSTIF 108 9 16 80 AMOWINSTIF 108 9 16 80 AMOWINSTIF 108 9 15 75 AMOWINSTIF 23 9 16 80 CIPIFOSWA 312 9 16 80 CLIFICALLI	YLHTLWKA 147 6 20 100 YLPLDKGI 122 8 20 100 YLPLDKGI 118 8 16 90 YLPLDKGI 640 8 19 95 YPALMPLY 521 9 19 95 ALCSVYRRA 58 9 18 90 ALLONGELM 58 9 18 90 ALMPLYACI 642 9 16 90 AMOWNSTTF 108 9 16 90 AMSTTOLE 108 9 15 75 APCALFISA 146 9 16 9 CIPLLVIL 239 9 20 100 CAPSYRING	%	WMCLRRFI	237	80	19	95	1686
YLPLDKGI 122 B 20 100 YLVSFGWW 118 B 18 90 YLVSFGWW 118 B 18 90 YPALMPLY 640 B 18 90 AICSVVRRA 521 9 18 90 AICSVVRRA 521 9 18 90 ALCNVGELM 54 9 18 90 ALLONGELM 54 9 18 90 ALLONGELM 54 9 19 95 ALLONGELM 54 9 19 95 ALMPLYACI 642 9 19 95 ALNOALICW 54 9 16 80 AMSTDLEA 102 9 15 75 APCNIFTSA 146 9 15 75 APCNIFTSA 102 9 16 100 CLIFLUALL 239 9 19 19 CLIFLUALL	YLPLDKGI 122 8 20 100 YLVSFGWW 118 8 10 100 YLVSFGWW 118 8 19 95 YPALMPLY 640 8 19 95 AICSVORRA 521 9 19 95 AICSVORRA 54 9 18 90 ALROALCW 54 9 18 90 ALROALCW 54 9 19 95 AMCWINSTIF 108 9 16 80 AMCONITION 54 9 16 80 AMCONITION 9 16 80 AMCONITION 9 16 80 AMCONITION 9 16 80 AMCONITION 9 16 80 CUIPARION 1 9 16 80 COLIPARION 7 9 16 80 COLIPARION 7 9 16 80	젍	YLHTLWKA	147	80	20	100	1687
YLVSFGWW 118 8 18 90 YPALMPLY 640 8 19 95 YPALMPLY 640 8 19 95 AICSVVRRA 521 9 15 75 AICSVVRRA 58 9 18 90 AILCWGELM 642 9 18 90 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 16 80 ALMOWNSTTF 108 9 16 80 ALMOWNSTTF 146 9 15 75 APOLITION 253 9 16 100 CLIFLUAL 253 9 19 100 CLIFLUAL 232 9 19 100 CPRYOMSK	YLVSFGWW 118 8 18 90 YPALMPLY 640 8 19 95 YPALMPLY 640 8 19 95 AICSVVRRA 521 9 18 90 AICSVVRRA 58 9 18 90 AILCWGELM 54 9 18 90 ALMPLYACI 642 9 19 95 ALMOMISTITE 108 9 16 80 AMSTTOLEA 146 9 15 75 APCHETSA 146 9 16 100 CLIFLUAL 253 9 19 19 CLIFLUAL 232 9 19 100 CRUPARINA 14 9 16 80 COLIFICATION	ಶ	YLPLDKGI	122	80	20	100	1688
YPALMPLY 640 8 19 95 YQHFRQL 5 1 75 75 AICSVVRRA 521 9 19 95 AICWGELM 58 9 18 90 ALMPLYACI 642 9 18 90 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 19 95 ALMOMINSTTF 108 9 16 80 AMSTTOLEA 102 9 15 75 APCINFTSA 146 9 15 75 APCINFTSA 312 9 20 100 CLIFLUAL 253 9 19 100 CLIFLUAL 239 9 19 9 CLIFLUAL 232 9 100 CPTYOASKL 14 9 16 80	YPALMPLY 640 8 19 95 YQHFRQL 5 1 75 75 AICSVVRRA 521 9 19 95 AICWGELM 58 9 18 90 ALMPLYACI 642 9 18 90 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 16 80 ALMPLYACI 642 9 16 80 ALMPLYACI 642 9 16 95 ALMOWNSTT 108 9 16 80 AMSTTOLEA 146 9 16 80 CIFLVIL 253 9 20 100 CLIFLUXIL 232 9 18 90 CASTORASKIL 14 9 16 80 COLIFICATION </td <td>SEC SEC</td> <td>YLVSFGVW</td> <td>118</td> <td>ω</td> <td>18</td> <td>06</td> <td>1689</td>	SEC SEC	YLVSFGVW	118	ω	18	06	1689
YOHFRIQL 5 8 15 75 AICSVVRRA 521 9 19 95 ALLOWGELM 58 9 18 95 ALMPLYACI 642 9 18 90 ALMPLYACI 642 9 18 95 ALMPLYACI 642 9 16 80 ALMPLYACI 54 9 16 80 ALROAICW 54 9 16 80 AMSTYDLEA 102 9 16 80 APCNIFTSA 146 9 15 75 APCNIFTSA 312 9 20 100 CLIFLUAL 253 9 19 9 CLRFIIII 239 9 19 9 CATRGETY 107 9 18 90 CPTYOASKIL 14 9 16 80	YOHFRIQL 5 8 15 75 AICSVVRRA 521 9 19 95 AILCWGELM 58 9 18 95 ALMPLYACI 642 9 18 90 ALMPLYACI 642 9 18 90 ALMPLYACI 642 9 16 90 ALMPLYACI 54 1 9 16 80 ALMOMNISTIF 108 9 16 80 AMOTONISTIF 108 9 15 75 APCNIFTSA 146 9 16 100 CLIFLUAL 253 9 20 100 CLIFLIAL 253 9 19 9 CLIFLIAL 239 9 19 9 CLIFLIAL 232 9 100 CPTYOASKIL 14 9 16 80 COLDPARDU 7 9 16 80	젒	YPALMPLY	640	60	19	95	1690
AICSVVRA 521 9 19 95 AILCWGELM 58 9 18 90 ALMPLYACI 642 9 18 90 ALMPLYACI 642 9 19 95 ALMPLYACI 54 9 16 80 AMONNISTIF 108 9 16 80 AMONNISTIF 102 9 15 75 AMONNISTIF 146 9 15 75 ACHILLAL 253 9 20 100 CLIFLLVIL 253 9 19 95 CLIFLINI 239 9 19 9 CLIFLINI 239 9 19 9 CATFGRETY 107 9 18 90 CPTVOASKIL 14 9 16 80	AICSVVRAA 521 9 19 95 ALLWELVACI 642 9 18 90 ALMPLYACI 642 9 18 90 ALMPLYACI 642 9 18 90 ALMPLYACI 54 9 19 95 ALMOMNISTIF 108 9 16 80 AMOMNISTIF 108 9 15 75 AMOMNISTIF 108 9 15 75 AMOMNISTIF 108 9 15 75 AMOMNISTIF 108 9 16 100 CIPILLAL 253 9 20 100 CLIFLAL 253 9 19 9 CLIFLAL 239 9 19 9 CATFGRETY 107 9 16 80 CONDARADO 7 9 16 80 CALDARDO 7 9 16 80	ಕ	YOHFFRUL	S	80	15	7.5	1691
AILCWGELM 58 9 18 90 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 19 95 ALMPLYACI 54 • 9 19 95 ALMOMINSTIF 108 9 16 80 AMOWINSTIF 102 9 15 75 AMSTIDLEA 102 9 15 75 AMSTIDLEA 146 9 16 160 CIPILLAL 253 9 20 100 CLARFIII 239 9 19 9 CATFGREIY 107 9 18 90 CPTVOASKL 14 9 16 80	AILCWGELM 58 9 18 90 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 19 95 ALMPLYACI 54 • 9 19 95 ALMPLYACI 108 9 16 80 AMOWINSTIF 102 9 15 75 AMSTIDLEA 102 9 15 75 AMSTIDLEA 146 9 16 100 CIPILAL 253 9 20 100 CLIFILIVIL 239 9 19 95 CLIFILIVIL 239 9 18 90 CATTGRETY 107 9 18 90 CATTGRETY 1 9 16 80 COLDPARDV 7 1 9 16 80	ಕ	AICSVVRRA	521	6	19	95	1692
ALMPLYACI 642 9 19 95 ALMOWNSTF 108 9 95 AMOWNSTF 108 9 95 AMOWNSTF 108 9 16 80 AMSTTOLEA 102 9 15 75 APCNFFTSA 146 9 20 100 CLIFLUL 253 9 100 CLRFIIL 239 9 19 CATFGRETY 107 9 18 CCPTVOASKL 14 9 16 80	ALMPLYACI 642 9 19 95 ALMOWNSTF 108 9 95 AMOWNSTF 108 9 16 80 AMSTTOLEA 102 9 15 75 AMSTTOLEA 102 9 15 75 CIPISSWA 312 9 20 100 CLIFLLVL 253 9 19 18 95 CLIFGREY 107 9 18 90 CCLDPARDY 7 1 9 16 80	27	AILCWGELM	58	ග	18	06	1693
ALROAILCW 54 , 9 19 95 AMQWNSTTF 108 9 16 80 AMSTTOLEA 102 9 15 75 APONFFSA 146 9 15 75 APONFFSA 312 9 20 100 CLIFLLVL 239 9 18 CLIFGREV 107 9 18 90 CPTVOASKL 14 9 16 80	ALROAILCW 54 , 9 19 95 AMQWNSTTF 108 9 16 80 AMSTTOLEA 102 9 15 75 APONFFSA 146 9 15 75 APONFFSA 312 9 20 100 CLIFILVIL 253 9 19 CLIFILVIL 239 9 19 CLTGREIV 107 9 18 90 CCLDPARDV 7 ! 9 16 80	ಕ್ಷ	ALMPLYACI	642	o	19	95	1694
AMOWNSTTF 108 9 16 80 AMSTTOLEA 102 9 15 75 APCNFTSA 146 9 15 75 APCNFTSA 146 9 16 75 CIPIPSSWA 312 9 20 100 CLIFILVIL 253 9 19 95 CLRFIIF 239 9 18 90 CATFGRETY 107 9 18 90 CPTVOASKL 14 9 16 80	AMOWNSTTF 108 9 16 80 ANSTTOLEA 102 9 15 75 APONFFISA 146 9 15 75 APONFFISA 146 9 16 75 CIPILYAL 253 9 20 100 CLIFILYAL 239 9 19 95 CLIFILYAL 239 9 18 90 CATGRIFIIT 232 9 18 90 CPTYOASKIL 14 9 16 80 COLDPARDV 7 1 9 16 80	STC STC	ALROAILCW	54	o	19	95	1695
AMSTTOLEA 102 9 15 75 APCNFFTSA 146 9 15 75 CIPISSWA 312 9 20 100 CLIFLUAL 253 9 20 100 CLRRFIIR 239 9 19 95 CLRGRETV 107 9 18 90 CPGYRWMCL 232 9 20 100 CPGYVOASKL 14 9 16 80	AMSTTOLEA 102 9 15 75 APCNFFTSA 146 9 15 75 CIPISSWA 312 9 20 100 CLIFLUAL 253 9 20 100 CLRRIIR 239 9 19 95 CLRGRETV 107 9 18 90 CPGYRWMCL 232 9 20 100 CPGYNDASKL 14 9 16 80	₩	AMOWNSTTF	108	6	16	80	1696
APCNFFTSA 146 9 15 75 CIPISSWA 312 9 20 100 CLIFLUAL 253 9 20 100 CLRRFIIR 239 9 19 95 CLRGRETV 107 9 18 90 CPGYRWMCL 232 9 20 100 CPGYVDASKL 14 9 16 80	APCNFFTSA 146 9 15 75 CIPIPSSWA 312 9 20 100 CLIFLUAL 253 9 20 100 CLRFIIR 239 9 19 95 CLTFGRETY 107 9 18 90 CPGYRWMCL 232 9 20 100 CPTVOASKL 14 9 16 80 COLDPARDY 7 1 9 16 80	×	AMSTTDLEA	102	O	15	7.5	1697
CIPIPSSWA 312 9 20 100 CLIFLUAL 253 9 20 100 CLARFIIR 239 9 19 95 CLIFGRETY 107 9 18 90 CPGYRWMCL 232 9 20 100 CPTVOASKL 14 9 16 80	CIPIPSSWA 312 9 20 100 CLIFLUAL 253 9 20 100 CLARFIIR 239 9 19 95 CLIFGRETY 107 9 18 90 CPGYRWMCL 232 9 20 100 CPTVOASKL 14 9 16 80 COLDPARDY 7 1 9 16 80	×	APCNFFTSA	146	O	15	7.5	1698
CLIFILVIL 253 9 20 100 CLARFIIR 239 9 19 95 QLTFGRETY 107 9 18 90 CPGYRWMCL 232 9 20 100 CPTVOASKL 14 9 16 80	CLIFILVIL 253 9 20 100 CLARFIIR 239 9 19 95 CLIFGRETY 107 9 18 90 CPGYRWMCL 232 9 20 100 CPTVDASKL 14 9 16 80 COLDPARDY 7 9 16 80	₩ M	CIPIPSSWA	312	o	20	100	1699
CLARFIIR 239 9 19 95 CLIFGRETY 107 9 18 90 CPGYRWMCL 232 9 20 100 CPTVOASKL 14 9 16 80	CLARFIIRL 239 9 19 95 CLIFGRETY 107 9 18 90 CPGYRWAMCL 232 9 20 100 CPTVOASKL 14 9 16 80 COLDPARDY 7 9 16 80	₩	CUFLIVIL	253	O	20	100	1700
CLIFGRETY 107 9 18 90 CPGYRWAMCL 232 9 20 100 CPTVOASKL 14 9 16 80	CLIFGRETY 107 9 18 90 CPGYRWAMCL 232 9 20 100 CPTVOASKL 14 9 16 80 CCLDPARDV 7 1 9 16 80	№	CLARFIIFL	239	o	19	95	1701
CPGYRWAMCL 232 9 20 100 100 CPTVQASKL 14 9 16 80	CPGYRWAMCL 232 9 20 100 CPTVQASKL 14 9 16 80 CQLDPARDV 7 9 9 16 80	SEC SEC	CLIFGRETV	107	o	18	06	1702
CPTVQASKL 14 9 16 80	CALDPARDV 7 1 9 16 80	A8	CPGYRWMCL	232	O	20	100	1703
	COLDPARDV 7 9 16 80	27	CPTVQASKL	14	O	16	80	1704

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
NUC	DLLDTASAL	29	6	17	85	1706
8	DUNGNILNV	40	o	19	95	1707
×	DPARDVLCL	10	6	16	80	1708
ಶ	DPSRGPLGL	778	6	18	06	1709
전	DVVLGAKSV	541	6	18	06	1710
₽N A	FIIFLFILL	243	6	16	80	1711
W ₀	FILLCLIF	248	O	16	80	1712
AG	FLFILLICL	246	o	16	80	1713
<u>ಷ</u>	FLLAQFTSA	513	6	19	95	1714
ೱ	FLSLGIM	562	ō	19	95	1715
PN BN	FLLTRILTI	183	6	16	80	1716
№	FPDHOLDPA	4	6	18	90	1717
8	FPHCLAFSY	530	o	. 19	98	1718
ğ	FPWI I GCAA	749	0	5	75	1719
	EVGI SPTVW	346	o	6	5 6	1720
	GICOVEADA	. 682	Ó	17	9 60	1721
	GLOGANDE	627	ď	. <u>-</u>	9 6	1722
	VC89/80170	62	o	÷ ÷) w	1793
: a	S SWOTEN	507	o	. 4	0 6	1724
2 2	TI LETTON	123		9 9	9 0	1725
} ⊊	0000X15	435	, σ	. .	o c	1726
չ չ	TO TO TO IT.	3		o .	2 6	1737
< 8	HLSLHGLFV	36 101	na	0 4	0 0	1211
2 8	HLYSHPIIL	- 6	n c	0 0	2 5	1730
걸 ;	HPAAMPHLL	674	n c	02	00.0	67/1
BW.	· IIFLFILLL	244	י מ	9	08	1730
	ILGFRKIPM	498	5 7 •	16	80	1731
₩	ILLICLIFL	249	o	20	100	1732
점	LRGTSFVY	760	o	16	80	1733
№	IPIPSSWAF	313	6	20	100	1734
M ₀	IPOSLDSWW	. 191	6	18	06	1735
젍	IVGLLGFAA	625	6	18	06	1736
ಶ	KLHLYSHPI	489	6	19	95	1737
절	KLIMPARFY	108	o	15	7.5	1738
젙	KVCORIVGL	620	o	17	85	1739
ಶ	KVGNFTGLY	55	თ	19	98	1740
절	LLAQFTSAI	514	o	19	95	1741
№	LICUFLY	251	თ	20	100	1742
2	LLDTASALY	30	თ	17	85	1743
절	LLGCAANWI	752	თ	16	80	1744
№	HIGHER	250	თ	20	100	1745
A	I PIFFC! W	378	G	20	100	1746
NC	JUSA ESTI	44	თ	19	95	1747
2	WS INSS I	407	თ	· -	06	1748
3 2	II M CAGEE	175	o	o	9 6	1749
<u>.</u>	TVBE/CAST	338		0 0	100	1750
;				,		
5	C	001	•	Q.	00	1751

Table XIV		HBV B6	HBV B62 Super Motif			
Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
ಭ	LPIHTAELL	712	σ	17	85	1753
×	LPVCAFSSA	58	6	19	95	1754
ಕ	LPVNRPIDW	611	6	16	80	1755
≥ 3	LVLLDYOGM	258	တာဇ	6 7	95	1756
<u>}</u> 8	LVLQAGFFL	336	, o			1758
	MMMMGPSI	360	0	2 -	9 69	1759
: 전	NEGNILNVSI	42	6	19	95	1760
점	NITSSNISM	406	. 6	18	06	1761
8	NLOSLTNLL	400	თ	20	100	1762
점 ;	NLSWLSLDV	411	တင	-8	06	1763
& &	PIFFCLWVY	380	. .	50	00r 9£	1764
ቷ ፳	PIHIAELLA	496	n σ	- 4	C C	1766
₫ ≩	PIPSSWAFA	314) (1)	5 4	0 60	1767
i දු	PLDKGIKPY	124	6	20	100	1768
ಕ್ಷ	PLEEDPR	20	o	19	95	1769
₩	PLLPIFFCL	377	6	20	100	1770
BN	PLLVLOAGF	174	6	. 19	95	1771
&	PLPIHTAEL	711	6	16	80	1772
ಶ	PMGVGLSPF	505	on (16	080	1773
2	PPAYRPPNA	129	an o	<u>6</u> ;	5 G	1774
S	PPHGGLLGW	o o	.	, ,	o 0	377
×ð	OLDPARDVL	187	ກ່ວ	0 4	0 0	1774
ā 2	RIVGLIGEA	624	. .	- -	06	1778
<u></u>	RLWDFSOF	376	6	19	56	1779
절	RVTGGVFLV	357	6	20	100	1780
AG M	SLDSWMTSL	194	6	19	98	1781
젚	SLDVSAAFY	416	တ	19	95	1782
₩	SLLVPFVOW	337	о	20	100	1783
젙 :	SLNFMGYVI	581	ത	15	75	1784
× 2	SLRGLPVCA	350	ത ദ	D 4	2 4 4 5	1786
3	SVRESMISI	330	. 6	9 9	080	1787
<u> </u>	TIPOSLDSW	190	6	18	06	1788
젍	TLWKAGILY	150	6	20	100	1789
젍	TPARVTGGV	354	6	18	06	1790
젒	TPTGWGLAI	691	o	15	7.5	1791
젍	TOCGYPALM	636	6	19	92	1792
3	TVQASKLCL	16	o	16	. 08	1793
≧	TVWLSVIWM	352	5 7 (5	75	1794
× :	VLCLRPVGA	ر د :	.	19	o 0	1795
×	ALGGCRING.	69	നന	1 1	O 60	1797
< d	VOINTEGE VALENCE	259	σ	. •	9 G	1798
3 6	VIOAGFRI	177	. 6	19	96	1799
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Table XIV

SEQ ID NO:	1800	1801	1802	1803	1804	1805	1806	1807	1808	1809	1810	1811	1812	1813	1814	1815	1816	1817	1818	1819	1820	1821	1822	1823	1824	1825	1826	1827	1829	1830	1831	1832	1833	1834	1835	1836	1837	1838	1839	1840	1841	1842	1843	1844	1845	1846
Conservancy (%)	85	80	90	56	100	50	56	06	06	9.6	7.5	06	95	95	95	100	06	85	7.5	80	85	06	85	95	95	080	0 6	900	o 55	85	95	9.6	06	92	95	7.5	85	06	9.2	98	80	95	7.5	85	80	080
Sequence	17	16	16	61	20	6-	6-	. 6	. 60	19	15	18	19	19	19	20	18	17	15	16	17	18	17	19	19	16	φ ,	0 4	. .	17	19	. 61	18	19	19	15	17	18	19	19	16	19	. 15	17	16	16
No. of Amino Acids	6	6	6	6	o	o	თ	o	თ	. თ	o	o	10	10	10	10	10	10	10	10	10	10	10	10	10	0.		<u> </u>	2 0	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
Position	741	759	751	414	335	237	393	118	538	. 640	cs.	768	521	633	516	312	533	23	239	7	622	31	53	14	E 4 6	243	246	171	513	14	530	346	132	57	509	348	29	29	19	173	203	123	699	429	495	497
Sequence	VLSRKYTSF	WILRGTSFV	WIEGCAANW	WI SI DVSAA	WI SLI VPFV	WMCIBBEIL	WPKFAVPNI	YI VSFGVWI	YMDDVVLGA	YPALMPLYA	YOHERMILL	YVPSALNPA	AICSVVRRAF	APFTQCGYPA	AQFTSAICSV	CIPIPSSWAF	CLAFSYMDDV	CLGWLWGMDI	CLRRFIIFLF	COLDPARDVL	CORINGLLGF	DIDPYKEFGA	DLLDTASALY	DVLCLRPVGA	· ELLSFLPSDF	FIFFILE	FILICIF	FUFILLED	FLUFTLACE	FPDHOLDPAF	FPHCLAFSYM	FVGLSPTVML	PALGGCRHAL.	GLPVCAFSSA	GLSPFLLAGF	GLSPTVWLSV	GMDIDPYKEF	GPCALRFTSA	GPLEEELPRL	GPLYLOAGF	GVGLSPFLLA	GVWIRTPPAY	HLNPNKTKRW	HPAAMPHLLV	HPIILGFRKI	III GEBKIPM
Protein	ಜ	젍	ğ	ğ	A	NG.	i 2	3	ಕ್ಷ	전	젍	8	젍	전		8	점	3	₩	×	젙	2	2	×	2	2 2	2 2	2 6	<u> </u>	3 8	ਲ	BW	×	×	ೱ	26	3	×	점	Se	젍	2	젒	젍	<u>ಕ</u>	5

Table XIV		HBV B6	HBV B62 Super Motif			
Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
2	ILLOUFIL	249	10	20	100	1847
젍	(LRGTSFVYV	092	10	16	80	1848
S	ILSTLPETTV	139	10	50	100	1849
2	IPIPSSWAFA	313	0 4	9- 9	80	1850
ಕ 8	IPMGVGLSPF	, C	0 0	0 6	200	1851
Z 5	IFWITH VENT	2 .	D C	17	9.5	1853
දූ ද	KI HI YSHPII	489	. 01	19	0 80	1854
점	KLPVNRPIDW	610	. 10	16	80	1855
젍	KOAFTFSPTY	653	10	19	95	1856
젒	KVCQRIVGIL	620	10	17	85	1857
×	KVLHKRTLGL	91	10	17	85	1858
8	LIFLYLLDY	254	10	19	98	1859
&	LLCLIFLLVL	251	10	20	100	1860
3	LLDYOGMLPV	260	10	18	06	1861
	LLGCAANWIL	752	10	16	80	1862
2	LLCLIFLLV	250	10	20	100	1863
≥	LPIFFCLWV	378	10	20	100	1864
2	LLSFLPSDFF	44	10	6	95	1865
2	LVLLDYQGM	257	0,	-	90	1866
<u> </u>	LINIOAGFFL	1/3	2 .	æ ;	0 0	1867
2 6	LLVPFVQWFV	338	0 0	5- 0	35	1868
3 6	PIFFCLWVY	213	2	7 7	001	1909
걸 >	LPIHIAELLA	51.7	2	<u> </u>	n c	1871
< ₹	ו איניזאט ול ו	123	2.00	20	100	1872
2 6	LVLLDYOGML	258	10	19	95	1873
8	LVLOAGFFLL	176	10	18	06	1874
8	MMWYWGPSLY	360	10	17	85	1875
젍	NITSSNIFSWL	406	10	18	90	1876
3	NLSVPNPLGF	15	10	15	7.5	1877
ಕ -	NPNKTKRWGY	571	10	5	7.5	1878
ස් :	NVSIPWTHKV	7 4 7	20,	50	100	1879
걸 중	PIDWKVCQHI	380		- 00	60	1881
\$ 6	A LINCTIO	713	01	- 5	2 4	2882
2 2	אים אים אים ואים ואים ואים ואים ואים ואי	124	0		5 5	1883
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3 €	PI GERDHO	10	. 01	<u> </u>	ິດ	1885
ಕ	PLHPAAMPHL	427	10	20	100	1886
8	PLLPIFFCLW	377	10	20	100	1887
8	PLLVLOAGFF	174	10	19	98	1888
젍	PLPIHTAELL	711	10	16	80	1889
젍	PLSYCHFRKL	2 ;	10	5	75	1890
ਲ (PLTVNEKRRL	86 30	o (17	ဆ	1891
로 :	PMGVGLSPFL	134	> C	9.0	200	1892
3	PPNAPILSTL	* 2	2	0.7	001	000

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Table XIV

QUAMERISCA 91 10 11 85 1884 RINGLLGFA 92 10 11 18 95 1885 RINGLLGFA 106 10 15 75 1895 RAUCINGE 54 10 11 18 96 1895 RAUCINGE 54 10 11 15 75 1895 SPHTALSOL 49 10 18 96 1895 SINGLANGE 54 10 18 96 1895 SINGLANGE 54 10 18 96 1895 SINGLANGE 43 10 18 96 1895 SINGLANGE 43 10 16 16 1895 1895 SINGLANGE 43 10 16 18 96 1895 SINGLANGE 43 10 16 18 96 1895 SINGLANGE 43 10 16 18 96 <t< th=""><th>Protein</th><th>Sequence</th><th>rosillon</th><th>No. of Amino Acids</th><th>Sequence</th><th>Conservancy (%)</th><th></th></t<>	Protein	Sequence	rosillon	No. of Amino Acids	Sequence	Conservancy (%)	
9.9		PVNRPIDWKV	612	10	17	85	1894
624 10 18 90 106 10 15 75 56 10 10 15 75 337 10 20 100 49 10 20 100 49 10 20 100 49 10 20 100 49 10 10 90 49 10 10 90 128 10 10 10 128 10 10 10 139 10 10 10 140 10 10 10 141 10 10 10 142 10 10 10 143 10 11 10 144 10 10 10 145 10 10 10 145 10 10 10 145 10 10 10 144 10 10 10 144 10 10 10		OLLWFHISOL	66	10	18	06	1895
106 10 15 75 56 10 18 75 818 10 18 75 44 10 19 95 403 10 19 95 403 10 18 90 330 10 16 16 330 10 16 18 330 10 16 80 330 10 16 80 340 10 16 80 340 10 16 80 340 10 17 85 414 10 17 85 424 10 16 80 425 10 17 85 43 10 11 85 44 11 10 11 95 44 11 11 19 95 44 11 11 11 11		RIVGLLGFAA	624	10	18	06	1896
56 10 18 90 818 10 15 75 337 10 20 100 493 10 20 100 493 10 18 90 493 10 18 90 350 10 16 80 384 10 18 90 193 10 18 90 194 10 18 90 195 10 16 80 194 10 18 90 194 10 19 95 195 10 10 15 194 10 11 16 80 195 10 10 16 80 195 10 10 10 10 10 195 10 10 10 10 10 10 250 10 10 10 1		RLKLIMPARF	106	10	15	7.5	1897
818 10 15 75 937 10 20 100 49 10 20 100 49 10 20 100 350 10 10 10 350 10 10 10 128 10 10 10 128 10 10 10 178 10 18 90 179 10 18 90 170 10 11 10 170 10 11 10 170 10 11 10 170 10 11 10 170 10 10 10 170 10 10 10 170 10 10 10 170 10 10 10 170 10 10 10 170 10 10 10 170 10 10 10 11 10 10 10		ROALCWGEL	26	10	18	06	1898
3.37 10 20 100 4.03 10 19 95 4.03 10 18 90 3.50 10 18 90 3.54 10 18 90 3.55 10 18 90 3.54 10 18 90 3.55 10 18 90 3.40 10 18 90 3.41 10 18 90 3.42 10 18 90 3.43 10 18 90 3.40 10 18 90 3.41 10 18 90 3.42 10 18 90 3.43 10 19 95 4.44 10 10 19 95 4.5 10 10 10 10 5.5 10 10 10 10 5.6 10 10 10 10 5.5 10 10 10 10 5.6 10 10 10 10 5.0 10 10 10 10 6.0 10 10 10		RVHFASPLHV	818	10	15	. 75	1899
54 10 19 95 403 10 18 90 49 10 20 100 350 10 16 10 190 10 18 90 178 10 18 90 178 10 18 90 133 10 18 90 143 10 19 95 17 10 19 95 17 10 19 95 17 10 10 10 18 90 10 10 19 95 10 10 10 10 10 10 26 10 10 10 26 10 10 10 26 10 10 10 26 10 10 10 26 10 10 10 26 10 10 10 26 10 10 10 27 <td></td> <td>SILVPFVOWF</td> <td>337</td> <td>10</td> <td>20</td> <td>100</td> <td>1900</td>		SILVPFVOWF	337	10	20	100	1900
403 403 403 404 405 406 407 408 409 409 409 409 409 409 409 409 409 409		SLRGLPVCAF	54	10	19	95	1901
49 10 20 100 350 10 16 80 354 10 18 90 190 10 18 90 543 10 18 90 543 10 18 90 133 10 18 90 340 10 19 95 370 10 19 95 414 10 19 95 759 10 19 95 751 10 19 95 751 10 19 95 751 10 19 95 751 10 19 95 751 10 19 95 751 10 19 95 751 10 19 95 752 10 10 10 753 11 11 19 95 752 11 11 10 11 752 11 11		SLTNLLSSNL	403	10	18	90	1902
350 10 15 75 190 10 18 90 154 10 18 90 178 10 18 90 179 95 10 18 90 170 10 14 90 17 85 170 10 14 90 17 85 17 17 85 17 17 17 85 17 17 18 17 18 </td <td></td> <td>SPHHTALROA</td> <td>49</td> <td>10</td> <td>20</td> <td>100</td> <td>1903</td>		SPHHTALROA	49	10	20	100	1903
330 10 16 80 190 10 18 90 128 10 18 90 57 10 18 90 53 10 17 85 133 10 18 90 340 10 18 90 340 10 18 90 525 10 16 80 759 10 16 80 751 10 16 80 751 10 16 80 751 10 16 80 751 10 16 80 752 10 17 85 753 10 17 85 853 10 11 19 95 853 11 11 19 95 853 11 11 19 95 853 11 11 19 95 853 11 11 19 95		SPTVWLSVIW	350	10	15	7.5	1904
190 10 18 90 354 10 18 90 128 10 18 90 543 10 15 75 133 10 18 90 340 10 18 90 398 10 19 95 17 10 16 80 525 10 10 16 80 759 10 17 85 17 751 10 16 80 17 85 10 10 16 80 86 10 10 17 85 144 10 17 85 17 145 10 17 85 17 145 11 19 95 17 145 11 19 95 11 146 11 11 19 95 140 11 11 19 95 140 11 11 11 <td< td=""><td></td><td>SVRFSWLSLL</td><td>330</td><td>10</td><td>16</td><td>80</td><td>1905</td></td<>		SVRFSWLSLL	330	10	16	80	1905
354 10 18 90 128 10 15 75 543 10 15 75 133 10 18 90 1340 10 18 90 340 10 19 95 17 85 10 17 85 17 10 16 80 17 17 10 16 80 17 18 10 17 85 17 19 10 17 85 17 14 10 17 85 17 14 10 17 85 17 14 10 17 85 17 14 11 19 95 17 14 11 19 95 17 14 11 19 95 11 14 11 11 19 95 14 11 11 19 95 14 11 11		TIPOSLDSWW	. 190	0-	18	06	1906
128 10 19 95 543 10 17 85 133 10 17 85 1340 10 18 90 340 10 19 95 17 10 16 80 525 10 17 85 751 10 16 80 751 10 16 80 751 10 16 80 751 10 17 85 751 10 17 85 751 10 17 85 752 10 17 85 753 10 17 85 754 10 17 85 85 10 10 10 85 10 10 10 85 10 11 10 85 11 11 10 85 11 11 10 85 11 11 10 <		TPARVTGGVF	354	10	18		1907
57 10 15 75 543 10 17 85 133 10 18 90 340 10 19 95 340 10 19 95 17 10 17 85 525 10 16 80 751 10 16 80 751 10 16 80 751 10 17 85 751 10 17 85 751 10 17 85 752 10 17 85 753 10 17 85 752 10 10 10 753 11 19 95 754 11 16 80 754 11 16 80 754 11 16 80 754 11 16 80 755 11 16 80 740 11 11 16 80		TPPAYRPPNA	128	10	19		1908
543 10 17 85 133 10 18 90 340 10 19 95 340 10 19 95 17 8 95 10 525 10 17 85 751 10 16 80 751 10 16 80 751 10 16 80 751 10 16 80 751 10 17 85 752 10 17 85 753 10 17 85 752 10 17 85 753 11 16 80 754 11 16 80 754 11 16 80 754 11 16 80 754 11 16 80 754 11 16 80 754 11 16 80 754 11 16 80		TPPHGGLLGW	57	10	15	7.5	1909
133 10 18 90 340 10 19 95 340 10 16 95 348 10 16 80 525 10 17 85 751 10 16 80 751 10 16 80 751 10 17 85 147 10 17 85 147 10 17 85 147 10 17 85 148 10 16 80 5 10 10 10 5 10 11 19 95 516 11 19 95 11 533 11 16 80 11 622 11 19 95 14 11 16 80 533 11 16 80 623 11 16 80 624 11 16 85 40 11 <t< td=""><td></td><td>VLGAKSVOHL</td><td>543</td><td>10</td><td>17</td><td>85</td><td>1910</td></t<>		VLGAKSVOHL	543	10	17	85	1910
340 10 19 95 398 10 16 86 17 10 17 85 525 10 10 16 80 759 10 16 80 17 414 10 16 80 17 414 10 17 85 17 237 10 17 85 17 447 10 20 100 10 263 10 17 85 11 5 10 18 96 11 533 11 19 95 11 533 11 19 95 11 622 11 11 16 80 11 623 11 11 16 80 11 533 11 11 16 80 11 623 11 11 16 80 11 624 11 11 19 95 11 7		VLGGCRHPLV	133	10	18		1911
398 10 19 95 740 10 17 85 525 10 19 95 759 10 16 80 751 10 16 80 751 10 19 95 751 10 17 85 80 10 17 85 147 10 17 85 147 10 17 85 148 90 16 10 149 95 11 19 95 149 11 19 95 11 140 11 19 95 11 140 11 19 95 11 140 11 11 16 85 140 11 11 16 85 140 11 11 16 85 140 11 11 16 85 140 11 11 16 85 140		VPFVQWFVGL	340	10	19		1912
17 10 16 80 740 10 17 85 525 10 19 95 751 10 16 80 751 10 16 80 751 10 17 85 237 10 17 85 147 10 17 85 147 10 18 96 5 10 18 96 633 11 19 95 516 11 19 95 517 11 16 80 533 11 16 80 512 11 19 95 14 11 16 80 622 11 17 85 14 11 16 80 43 11 16 80 246 11 16 80 11 16 80 11 14 11 16 80 <td< td=""><td></td><td>VPNLQSLTNL</td><td>398</td><td>10</td><td>19</td><td>95</td><td>1913</td></td<>		VPNLQSLTNL	398	10	19	95	1913
740 10 17 85 759 10 16 80 751 10 16 80 414 10 19 95 414 10 17 85 237 10 17 85 147 10 17 85 147 10 17 85 147 10 18 90 5 10 18 90 516 11 19 95 516 11 19 95 337 11 18 90 533 11 18 95 14 11 19 95 14 11 16 80 40 11 16 80 43 11 16 80 246 11 16 80 11 16 80 11 14 11 16 80 246 11 11 95 <td< td=""><td></td><td>VOASKLCLGW</td><td>17</td><td>10</td><td>16</td><td>. 80</td><td>1914</td></td<>		VOASKLCLGW	17	10	16	. 80	1914
525 10 19 95 759 10 16 80 751 10 19 95 414 10 17 85 26 10 17 85 147 10 17 85 147 10 17 85 147 10 18 90 5 10 18 90 633 11 19 95 516 11 19 95 516 11 19 95 307 11 19 95 11 19 95 11 623 11 19 95 14 11 19 95 14 11 19 95 14 11 19 95 14 11 19 95 14 11 19 95 14 11 19 95 14 11 19 95 14		WLSRKYTSF	740	10	17	85	1915
759 10 16 80 414 10 19 95 414 10 17 85 26 10 17 85 359 10 17 85 147 10 17 85 147 10 17 85 147 10 18 90 140 11 19 95 141 11 19 95 14 11 16 80 14 11 16 80 14 11 16 85 14 11 16 85 14 11 16 85 40 11 16 85 246 11 19 95 246 11 16 80 246 11 16 80 256 11 19 95 11 19 95 11 256 11 19 95 <td< td=""><td></td><td>WARAFPHCL</td><td>525</td><td>. 01</td><td>19</td><td>9.2</td><td>1916</td></td<>		WARAFPHCL	525	. 01	19	9.2	1916
751 10 16 80 414 10 19 95 26 10 17 85 147 10 17 85 147 10 17 85 147 10 18 90 15 10 15 75 633 11 19 95 516 11 19 95 516 11 19 95 312 11 16 80 533 11 16 80 14 11 16 80 622 11 17 85 14 11 17 85 43 11 19 95 246 11 19 95 246 11 19 95 11 19 95 11 19 95 11 19 95 246 11 19 95 11 19 95 <td< td=""><td></td><td>WILRGTSFVY</td><td>759</td><td>10</td><td>16</td><td>80</td><td>1917</td></td<>		WILRGTSFVY	759	10	16	80	1917
414 10 19 95 26 10 17 85 237 10 17 85 147 10 17 85 147 10 12 95 143 11 19 95 516 11 19 95 312 11 19 95 312 11 16 80 533 11 16 80 253 11 16 80 40 11 16 86 40 11 16 86 43 11 16 80 246 11 19 95 44 11 19 95 246 11 19 95 256 11 19 95 11 19 95 11 19 95 11 19 95 11 19 95 11 95 11 <td< td=""><td></td><td>· WLLGCAANWI</td><td>751</td><td>10</td><td>16</td><td>80</td><td>1918</td></td<>		· WLLGCAANWI	751	10	16	80	1918
26 10 17 85 237 10 19 95 359 10 17 85 147 10 20 100 263 10 18 90 516 11 19 95 312 11 19 95 312 11 16 80 253 11 16 80 253 11 16 80 40 11 16 85 40 11 19 95 43 11 19 95 246 11 19 95 256 11 16 80 278 11 19 95 43 11 19 95 246 11 16 80 256 11 16 80 256 11 19 95 11 19 95 256 11 19 95 11 19 95 11 19 95 11 19 95 12 95 11 13 95 11 <td></td> <td>WLSLDVSAAF</td> <td>414</td> <td>10</td> <td>19</td> <td>92</td> <td>1919</td>		WLSLDVSAAF	414	10	19	92	1919
237 10 19 95 11 14 15 15 16 17 18 15 17 18 18 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18		WLWGMDIDPY	56	10	17	82	1920
359 10 17 85 147 10 20 100 263 10 18 90 5 10 15 75 633 11 19 95 397 11 19 95 312 11 16 80 533 11 16 80 253 11 19 95 14 11 16 80 622 11 16 86 43 11 19 95 246 11 19 95 11 16 80 256 11 16 80 266 11 16 80 256 11 16 80 256 11 16 80 256 11 16 80 256 11 19 95 11 16 80 11 256 11 19 95 11 19 95 11 11 19 95 11 11 19 95 11 11 95 11 <tr< td=""><td></td><td>WMCLRRFIIF</td><td>237</td><td>10</td><td>19</td><td>95</td><td>1921</td></tr<>		WMCLRRFIIF	237	10	19	95	1921
147 10 20 100 263 10 18 90 633 11 19 95 516 11 19 95 397 11 19 95 533 11 16 80 53 11 19 95 14 11 19 95 14 11 16 80 40 11 17 85 43 11 19 95 246 11 16 80 256 11 16 80 11 16 80 12 95 11 246 11 16 80 256 11 19 95 11 16 80 11 14 11 16 80 256 11 19 95 11 19 95 11 19 95 11 19 95 11 95 11 11 19 95 11 95 11 12 95 11 13 11		WMMWYWGPSL	359	10	17	82	1922
263 10 18 90 5 10 15 75 633 11 19 95 516 11 19 95 397 11 16 80 533 11 16 80 253 11 19 95 14 11 16 80 40 11 17 85 43 11 19 95 246 11 16 80 246 11 16 80 256 11 16 80		YLHTLWKAGI	147	10	20	100	1923
5 10 15 75 633 11 19 95 516 11 19 95 397 11 16 80 312 11 16 80 533 11 19 95 14 11 16 80 14 11 16 80 40 11 19 95 43 11 19 95 246 11 16 80 44 11 16 80 256 11 16 80 11 16 80 11 256 11 16 80 11 16 80 11 256 11 19 95		YOGMLPVCPL	263	10	18	06	1924
633 11 19 95 11 19 35 11 19 35 11 19 35 11 19 35 11 19 35 11 11 19 35 11 11 11 11 11 11 11 11 11 11 11 11 11		YOHFRKILL	ις	10	15	7.5	1925
516 11 19 95 397 11 19 95 312 11 16 80 533 11 18 90 253 11 19 95 14 11 16 80 40 11 17 85 43 11 19 95 246 11 16 80 256 11 16 80 11 16 80 11 16 80 256 11 19 95 11 16 80 11 16 80 11 16 80 11 16 80 12 95 11 13 95 11 14 11 16 80 15 95 11 16 95 11 17 16 80 11 16 95 11 17 16 80 11 18 95 11 19 95 11 10 95 11 11 95 1		APFTOCGYPAL	633	=	19	95	1926
397 11 19 95 312 11 16 80 533 11 18 90 253 11 19 95 14 11 16 80 622 11 17 85 40 11 19 95 43 11 19 95 246 11 16 80 11 16 80 256 11 19 95 11 16 80 1 256 11 19 95		AGFTSAICSVV	516	=	19	95	1927
312 11 16 80 533 11 18 90 253 11 19 95 14 11 16 80 622 11 17 85 40 11 19 95 248 11 16 80 246 11 16 80 256 11 19 95 11 16 80 11 256 11 19 95		AVPNLOSLTNL	397		19	98	1928
533 11 18 90 1 253 11 19 95 1 14 11 15 75 1 622 11 17 85 1 40 11 19 95 1 248 11 16 80 1 256 11 19 95 1 256 11 19 95 1		CIPIPSSWAFA	312	=	16	80	1929
253 11 19 95 239 11 15 75 14 11 16 80 622 11 19 95 43 11 19 95 248 11 16 80 256 11 19 95 11 16 80 1 256 11 19 95		CLAFSYMDDVV	533	Ξ	- 8	06	1930
239 11 15 75 14 11 16 80 622 11 17 85 40 11 19 95 43 11 19 95 248 11 16 80 246 11 16 80 11 16 95 11 16 95 11 16 95 11 19 95		CLIFLYLLDY	253	=	19	. 95	1931
14 11 16 80 622 11 17 85 40 11 19 95 43 11 19 95 248 11 16 80 246 11 16 80 11 19 95		CLRRFIIFLFI	239	Ξ	15	7.5	1932
622 11 17 85 1 40 11 19 95 1 43 11 19 95 1 248 11 16 80 1 246 11 16 80 1 256 11 19 95 1		CPTVQASKLCL	14		16	80	1933
40 11 19 95 1 43 11 19 95 1 248 11 16 80 1 246 11 16 80 1 256 11 19 95 1		CORIVGLLGFA	. 625		17	85	1934
43 11 19 95 1 248 11 16 80 1 246 11 16 80 1 256 11 19 95 1		DLNLGNLNVSI	40		19	9.2	1935
248 11 16 80 1 246 11 16 80 1 256 11 19 95 1		ELLSFLPSOFF	43	=	19		1936
246 11 16 80 1 256 11 19 95 1		FILLCUFIL	248	1	16		1937
256 11 19 95 1		FIFILLCUF	246	11	16	80	1938
		FLLVLDYOGM	256	<u>.</u>	19	95	1939

Position No. of Amino Acids
132
766
348
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52
491
244
249
139
188
504
625
503
489
251
200
000
970
257
175
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379
712
123
611
178
939
433
-
42
411
774
6
616
496
138
427
377
174
711
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505
129

HBV B62 Super Motif

Table XIV

SEQ ID NO:		1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2013	2010	100	2018	5018	2020	2021	2022	2023	2024	2025	2026	2027
Conservancy	(%)	80	06	80	95	7.5	80	100	06	0 6 ;	06	7.5	100	95	98	100	92	100	7.5	80	85	95	06	95	080	06	80 G	ი ი ი	0 0	n c	0 0	C 6	0.0	080	95	100	92	82	100	100	9.0
Sequence	Frequency	16	18	16	19	15	16	20	18	18	18	15	20	19	19	20	19	20	15	16	17	19	8 :	6 9	16	æ :	17	5 0	₽ ¢	n •	9 9	5	0	16	19	20	19	17	20	20	0 +
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Position		106	192	œ	685	106	615	133	56	86	36	818	49	194	337	44	511	49	350	330	739	524	354	636	16	862	141	390	243		246	070	807	751	414	335	237	359	147	122	640
Sequence		POAMOWNSTTF	POSLDSWWTSL	CILDPARDVICL	QVFADATPTGW	RLKLIMPARFY	RPIDWKVCQRI	RPPNAPILSTL	ROALCWGELM	ROLLWFHISCL	RVAEDLNLGNL	RVHFASPLHVA	SIPWTHKVGNF	SLDSWMTSLNF	SLLVPFVQWFV	SPEHCSPHHTA	SPFLLAOFTSA	SPHHTALROAI	SPTVWLSVIWM	SVRFSWLSLLV	SWLSRKYTSF	SWRRAFPHCL	TPARVTGGVFL	TOCGYPALMPL	TVOASKLCLGW	· VLLDYOGMLPV	VLSRKYTSFPW	VPNLOSLINIL	VOASKLCLGWL	VCWFVGLSP1V	VVLGARSVCHL	VVHKAFFHCLA	WILRGTSFVYV	WLLGCAANWIL	WLSLDVSAAFY	WLSLLVPFVQW	WMCLRRFIIFL	WMMWWGPSLY	YLHTLWKAGIL	YLPLDKGIKPY	JAN IMM MAY
Protein		₩ W	&	×	젍	હ	젙	SZ.	SAC SAC	SEC SEC	적	전	점	8	2	SEC SEC	ಶ	3	M M	2	ಕ್ಷ	젍	절:	전 :	2		호 8	₹ :	₹ 8	š š	2 8	₹ 8	₫ ;	전 :	ದ	№	BN BN	AN M	전	점	<u>د</u>

HBV A01 Motif with Binding Information

Position Sequence AA A*0101 166 ASFCGSPY 8 0.0001 737 DNSVULSRYY 10 0.0001 630 GFAAPTOCGY 11 0.0680 630 GFAAPTOCGY 11 0.0680 630 GFAAPTOCGY 11 0.0680 653 GCRETYLEY 8 0.1100 653 KOAFTSPTY 10 0.1100 653 LLDTASALY 9 12.0000 415 LSLDVSAFY 10 0.0150 137 LITGRETYLEY 11 0.0150 137 LITGRETYLEY 11 0.0150 103 MSYNUSRKY 9 0.2100 738 NAVISRKY 9 0.2100 737 PIDKGIKPY 10 0.1700 737 PIDCGSPY 9 0.2100 738 SASFCGSPY 9 0.2100 738 VIGHTSRYY 11 0.3200 738 V			:				
166 ASFCGSPY 8 737 DNSWLSRKY 10 0.0001 631 FAAPFTGCGY 10 0.0680 630 GFAAPTGCGY 11 0.0680 630 GREIVLEY 8 0.0680 630 GREIVLEY 8 0.0680 653 KOAFTSPTY 10 0.1100 653 KOAFTFSPTY 10 0.0150 415 LLDTASALY 9 12.0000 415 LLGDASALY 9 0.0150 103 MATTOLEAY 9 0.8500 103 MSTOLEAY 9 0.2100 124 PLDKGIKPY 10 0.1700 124 PLDKGIKPY 9 5.2000 165 SASFCGSPY 9 5.2000 165 SASFCGSPY 9 5.2000 104 STTDLEAY 1 1 59 WAMANYWGPSLY 11 0.3200 640 YSLNFMGY 8	Freq.	Protein	Position	Sequence	AA	A*0101	SEQ ID NO:
737 DNSVVLSRKY 10 0.0001 631 FAAPFTOCGY 10 0.0680 630 GFAAPFTOCGY 10 0.0680 140 GRETVLEY 8 0.0680 579 GYSLNFMGY 9 0.1100 653 KOAFTFSPTY 10 0.0001 415 LLDTASALY 9 12.0000 415 LLDTASALY 9 12.0000 415 LLDTASALY 9 0.0150 137 LTFGRETVLEY 11 0.0150 138 MSTTOLEAY 9 0.0150 124 PLDKGIRPY 9 0.0005 124 PLDKGIRPY 9 0.2100 797 PTGRTSLY 9 5.2000 165 SASFCGSPY 9 5.2000 104 STTDLEAY 11 0.3200 414 WLSLDVSAFY 11 0.3200 580 YSLNFMGY 8 11 0.3200	20	젒	166	ASFCGSPY	ω		2028
631 FAAPFTOCGY 10 0.0680 630 GFAAPTOCGY 11 640 GARTALEY 8 579 GYSLNFMGY 9 149 HTLWRAGILY 10 0.0100 653 LLDTASALY 10 0.0001 30 LLDTASALY 10 0.0001 415 LSLDVSAAFY 10 0.0150 137 LTFGRETALEY 11 138 MSYTDLEAY 9 0.8500 124 PLDKGIRPY 9 0.01700 124 PLDKGIRPY 9 0.01700 124 PLDKGIRPY 9 0.2100 125 SASFCGSPY 9 5.2000 165 SASFCGSPY 9 5.2000 165 SASFCGSPY 9 6.02100 164 STTDLEAY 8 11 0.3200 164 WLSLDVSAAFY 11 0.3200 178 WLSLDVSAAFY 11 0.3200	18	점	737	DNSVVLSRKY	10	0.0001	2029
630 GFAAPTOCGY 11 140 GRETVLEY 8 579 GYSLNFMGY 9 149 HTLWKAGILY 10 0.1100 653 KOAFTFSPTY 10 0.0001 415 LLDTASALY 9 12.0000 415 LLDTASALY 9 0.0150 137 LLDTASALY 9 0.0150 138 MANNYMGPSLY 10 0.0810 MSTTDLEAY 9 0.0005 124 PLDKGIKPY 9 0.0005 124 PLDKGIKPY 9 0.1700 737 PTGRTSLY 9 0.2100 738 SASFCGSPY 9 0.2100 7416 SLDVSAAFY 9 5.2000 104 STTDLEAY 8 414 WLSLDVSAAFY 11 0.3200 790 YPALMPLY 8 640 YPALMPLY 8 580 YSLNFMGY 8	19	점	631	FAAPFTOCGY	10	0.0680	2030
140 GRETVLEY 8 579 GYSLNFMGY 9 149 HTLWKAGILY 10 0.1100 653 KQAFTESPTY 10 0.0001 30 LLDTASALY 9 12.0000 415 LLDVSAAFY 10 0.0150 137 LTFGRETVLEY 11 0.0150 103 MAMAYWAGELY 9 0.8500 738 MSYLSRKY 9 0.8500 738 NSVLSRKY 9 0.0005 738 NSVLSRKY 9 0.2100 738 NSVLSRKY 9 0.2100 738 PLDKGIKPY 10 0.1700 797 PTGRTSLY 9 0.2100 8 SASFCGSPY 9 5.2000 164 STDLEAY 8 8 798 TTGRTSLY 8 8 790 VPALMPLY 8 8 80 VSLNFMGY 8 8	19	ೱ	630	GFAAPFTQCGY	=		2031
579 GYSUNFMGY 9 149 HTLWKAGILY 10 0.1100 653 KQAFTFSPTY 10 0.0001 30 LLDTASALY 9 12.0000 415 LSLDVSAAFY 10 0.0150 137 LTFGRETVLEY 11 0.0150 103 MANYWGPSLY 10 0.0810 103 MSTTDLEAY 9 0.8500 738 NSVLSRKY 9 0.2100 739 PTTGRISLY 9 0.2100 797 PTTGRTSLY 9 5.2000 165 SASFCGSPY 9 5.2000 104 STTDLEAY 8 5.2000 104 STDLEAY 8 6 414 WLSLDVSAAFY 9 5.2000 590 VPALMPLY 8 6 640 VPALMPLY 8 6 640 VSLNFMGY 8 6	15	2	140	GRETVLEY	&		2032
149 HTLWKAGILY 10 0.1100 653 KQAFTSPTY 10 0.0001 30 LLDTASALY 9 12.0000 415 LSLDVSAAFY 10 0.0150 137 LTFGRETVLEY 11 0.0150 103 MAMYYWGPSLY 10 0.0810 NSVLSRKY 9 0.8500 738 NSVLSRKY 9 0.0005 124 PLDKGIKPY 10 0.1700 797 PTTGRTSLY 9 0.2100 165 SASFCGSPY 9 5.2000 104 STTDLEAY 8 5.2000 104 STTDLEAY 8 5.2000 104 WASLDVSAAFY 11 0.3200 640 YPALMPLY 8 640 YPALMPLY 8 580 YSLNFMGY 8 6000 6000	17	ಶ	579	GYSLNFMGY	6		2033
653 KQAFTSPTY 10 0.0001 30 LLDTASALY 9 12.0000 415 LSLDVSAAFY 10 0.0150 137 LTFGRETVLEY 11 0.0150 103 MSTTDLEAY 9 0.8500 738 NSVVLSRKY 9 0.0005 124 PLDKGIKPY 9 0.0005 124 PLDKGIKPY 9 0.2100 797 PTTGRTSLY 9 0.2100 165 SASFCGSPY 9 9 0.2100 165 SASFCGSPY 9 9 5.2000 164 STTDLEAY 8 8 17GRTSLY 8 8 17GRTSLY 8 8 11 WLSLDVSAAFY 11 0.3200 640 YPALMPLY 8 8	20	점	149	HTLWKAGILY	10	0.1100	2034
30 LLDTASALY 9 12.0000 415 LSLDVSAAFY 10 0.0150 137 LTFGRETVLEY 11 360 MMMVYWGPSLY 10 0.0810 103 MSTTDLEAY 9 0.8500 738 NSVVLSRKY 9 0.0005 124 PLDKGIKPY 9 0.1700 797 PTTGRTSLY 9 0.2100 165 SASFGSPY 9 0.2100 165 SASFGSPY 9 5.2000 104 STTDLEAY 8 8 11 WLSLDVSAAFY 11 0.3200 640 YPALMPLY 8 8	19	점	653	KOAFTFSPTY	0.	0.0001	2035
415 LSLDVSAAFY 10 0.0150 137 LTFGRETVLEY 11 0.0810 360 MAMWYWGPSLY 10 0.0810 103 MSTDLEAY 9 0.8500 738 NSVVLSRKY 9 0.0005 124 PLDKGIKPY 10 0.1700 797 PTTGRTSLY 9 0.2100 797 SASFCGSPY 9 5.2000 104 STTDLEAY 8 5.2000 798 TTGRTSLY 8 5.2000 414 WLSLDVSAAFY 11 0.3200 640 YPALMPLY 8 41 580 YSLNFMGY 8 8	17	3	30	LLDTASALY	6	12.0000	2036
137 LTFGRETVLEY 11 360 MAMAYWGPSLY 10 0.0810 103 MSTTDLEAY 9 0.8500 738 NSVVLSRYY 9 0.0005 124 PLDKGIKPY 10 0.1700 797 PTTGRTSLY 9 0.2100 797 SASFGSPY 9 5.2000 165 SASFGSPY 9 5.2000 104 STTDLEAY 8 5.2000 798 TTGRTSLY 8 11 414 WLSLDVSAAFY 11 0.3200 640 YPALMPLY 8 11 580 YSLNFMGY 8 8	19	점	415	LSLDVSAAFY	10	0.0150	2037
360 MMMVYWGPSLY 10 0.0810 103 MSTTDLEAY 9 0.8500 738 NSVVLSRYY 9 0.0005 124 PLDKGIKPYY 10 0.1700 797 PTTGRTSLY 9 0.2100 165 SASFCGSPY 9 5.2000 416 SLDVSAAFY 9 5.2000 104 STTDLEAY 8 5.2000 798 TTGRTSLY 8 414 414 WLSLDVSAAFY 11 0.3200 640 YPALMPLY 8 580 YSLNFMGY 8	15	3	137	LTFGRETVLEY	=		2038
103 MSTTDLEAY 9 0.8500 738 NSVVLSRKY 9 0.0005 124 PLDKGIKPY 10 0.1700 797 PTTGRTSLY 9 0.2100 165 SASFCGSPY 9 0.2100 416 SLDVSAAFY 9 5.2000 104 STTDLEAY 8 5.2000 798 TTGRTSLY 8 11 414 WLSLDVSAAFY 11 0.3200 640 YPALMPLY 8 580 YSLNFMGY 8	17	8	360	MMWYWGPSLY	10	0.0810	2039
738 NSVVLSRKY 9 0.0005 124 PLDKGIKPY 9 0.1700 797 PTTGRTSLY 9 0.2100 165 SASFGSPY 9 0.2100 416 SLDVSAAFY 9 5.2000 104 STTDLEAY 8 5.2000 798 TTGRTSLY 8 11 414 WLSLDVSAAFY 11 0.3200 640 YPALMPLY 8 11 580 YSLNFMGY 8 8	15	×	103	MSTTDLEAY	6	0.8500	2040
124 PLDKGIKPY 9 124 PLDKGIKPYY 10 0.1700 797 PTTGRTSLY 9 0.2100 165 SASFGSPY 9 5.2000 416 SLDVSAAFY 9 5.2000 104 STTDLEAY 8 7.2000 798 TTGRTSLY 8 8 414 WLSLDVSAAFY 11 0.3200 640 YPALMPLY 8 8 580 YSLNFMGY 8 8	18	젒	738	NSVVLSRKY	6	0.0005	2041
124 PLDKGIKPYY 10 0.1700 797 PTTGRTSLY 9 0.2100 165 SASFGSPY 9 5.2000 416 SLDVSAAFY 9 5.2000 104 STTDLEAY 8 7.2000 798 TTGRTSLY 8 8 414 WLSLDVSAAFY 11 0.3200 640 YPALMPLY 8 8 580 YSLNFMGY 8 8	20	ಶ	124	PLDKGIKPY	6		2042
797 PTTGRTSLY 9 0.2100 165 SASFGSPY 9 5.2000 416 SLDVSAAFY 9 5.2000 104 STTDLEAY 8 7.2000 798 TTGRTSLY 8 11 414 WLSLDVSAAFY 11 0.3200 599 YPALMPLY 8 7.200 580 YSLNFMGY 8 8	20	젒	124	PLDKGIKPYY	10	0.1700	2043
165 SASFGGSPY 9 5.2000 416 SLDVSAAFY 9 5.2000 104 STTDLEAY 8 7 798 TTGRTSLY 8 8 414 WLSLDVSAAFY 11 0.3200 599 YPALMPLY 8 8 580 YSLNFMGY 8	17	절	797	PTTGRTSLY	တ	0.2100	2044
416 SLDVSAAFY 9 5.2000 104 STTDLEAY 8 5.2000 798 TTGRTSLY 8 8 414 WLSLDVSAAFY 11 0.3200 559 VPALMPLY 8 8 580 YSLNFMGY 8	20	점	165	SASFCGSPY	ത		2045
104 STTDLEAY 8 798 TTGRTSLY 8 414 WLSLDVSAAFY 11 359 WMMWYWGPSLY 11 0.3200 640 YPALMPLY 8 580 YSLNFMGY 8	19	점	416	SLDVSAAFY	6	5.2000	2046
798 TTGRTSLY 8 414 WLSLDVSAAFY 11 359 WMMWYWGPSLY 11 0.3200 640 YPALMPLY 8 580 580 YSLNFMGY 8	15	×	104	STTDLEAY	80		2047
414 WLSLDVSAAFY 11 359 WMMWYWGPSLY 11 0.3200 640 YPALMPLY 8 580 580 YSLNFMGY 8		절	798	TTGRTSLY	80		2048
359 WMMWYWGPSLY 11 0.3200 640 YPALMPLY 8 580 YSLNFMGY 8	19	젙	414	WLSLDVSAAFY	Ξ		2049
640 YPALMPLY 8 580 YSLNFMGY 8	17	<u>₹</u>	359	WMMWYWGPSLY	Ξ	0.3200	2050
580 YSLNFWGY 8	19	헍	640	YPALMPLY	æ		2051
	17	헏	580	YSLNFMGY	æ		2052

TABLE XV

Table XVI HBV A03 Motif With Binding

CONSERVATION Freq. Fred. Fred. <th></th> <th></th> <th></th> <th></th> <th>DEV AUS MOUI WILL BINGING</th> <th></th> <th></th> <th></th>					DEV AUS MOUI WILL BINGING			
POL 721 AAGENERS 8 0,0004 POL 722 AAGENERSGA 11 0,0004 POL 632 AAPFTOCKY 10 0 POL 722 AAPFTOCKY 11 0 POL 722 AAPFTOCKY 11 0 POL 529 AAPFTOCKY 8 0 POL 529 AFFHOLLAFSY 10 0 POL 529 AFFHOLLAFSY 11 0 POL 529 AFFHOLLAFSY 10 0 POL 625 AFFHOLLAFSY 11 0 POL 635 AFFHOLLAFSY 11 0 POL 635 AFFHOLLAFSY 11 0 POL 635 AFFRONTAFF 11 0 POL 635 AFFRONTAFF 11 0 POL 635 AFFRONTAFF 11 0 POL 521 ACSANTRAF 10 0	ancy	Freq.	Protein	Position	Sequence	АА	A'0301	SeqID Num
POL 721 AACFARSSCA 11 POL 632 AAPPTOCOST 9 POL 632 AAPPTOCOST 10 POL 722 AAPPTOCOST 11 POL 726 AAPPTOCOST 11 POL 776 AAPPTOCOST 10 POL 529 APPTOCAMP 8 POL 625 APPTOCAMP 11 POL 655 APPTOCAMP 11 POL 657 APPTOCAMP 10 POL 657 AAPPTOCAMP 10 <td></td> <td>. 17</td> <td>Pot</td> <td>721</td> <td>AACFABSB</td> <td>ω</td> <td>0.0004</td> <td>2053</td>		. 17	Pot	721	AACFABSB	ω	0.0004	2053
POL 632 AMPTICOCK 1 POL 722 AMPTICOCK 11 POL 728 AGAGRISCARA 10 POL 529 AFPICIORIA 8 POL 529 AFPICIARY 10 POL 655 AFRICALARY 9 X 62 AFRICALARY 9 POL 655 AFRICALARY 9 POL 655 AFRICALARY 10 POL 655 AFRICALARY 11 POL 655 AFRICALARY 9 POL 655 AFRICALARY 10 POL 655 AFRICALARY 10 POL 655 AFRICALARY 9 POL 655 AFRICALARY 9 POL 656 AGRICALARY 10 POL 657 ALFESPINAR 1 POL 657 AGRICALARY 1 POL 657 AGRICALARY 1		17	Pol	721	AACFARSRSGA	11		2054
POL 78.2 AAPPICOSPPA 11 POL 78.2 AACKPSSSGA 10 POL 52.9 APPICAFE 8 POL 52.9 AFPICAFE 8 POL 52.9 AFPICAFE 8 POL 65.5 AFFISHYK 9 POL 52.1 AACSWIRH 10 NACSWIRH 10 AACSWIRH 10 POL 52.1 AACSWIRH 10 NAC 52.1 AACSWIRH 10 AACSWIRH AACSWIRH 10		19	PQL	632	AAPFTQCGY	თ		2055
POL 722 ACFASRSCA 10 POL 776 ACDCPSTGA 11 POL 776 ACDCPSTGA 11 POL 529 AFFHCLAFSY 10 POL 529 AFFHCLAFSY 10 POL 655 AFTRSTYK 9 0.2600 POL 521 AGPCALPT 8 0.0002 POL 521 AGPCALPT 8 0.0002 POL 521 AGPCALPT 8 0.0002 NC 41 AGPCALPT 8 0.0004 NC 41 AGPCALPT		19	POL	632	AAPFTQCGYPA	11		2056
POL 688 MOMPTGWOLA 11 POL 578 ADDRTGWALASY 10 POL 529 AFPHCLAF 8 POL 529 AFPHCLAF 10 POL 655 AFREGARA 9 POL 655 AFTESPTY 9 0.2600 POL 66 AGPCALIFF 11 0.0002 NC 41 AGENCERIFYAR 9 0.0002 NC 521 AGCNARAR 10 0.0003 NC 41 AGCNARAR <td></td> <td>17</td> <td>전</td> <td>722</td> <td>ACFARSRSGA</td> <td>10</td> <td></td> <td>2057</td>		17	전	722	ACFARSRSGA	10		2057
POL 776 ADDPSRGA 8 POL 529 AFPICATESY 10 X 62 AFSSAGPCA 11 X 62 AFTSSPTY 10 POL 655 AFTSSPTY 10 POL 656 AFTSSPTY 10 POL 657 AFTSSPTY 10 POL 657 AFTSSPTY 10 AGPALIFR 8 0.0004 POL 521 AGSVARP 10 POL 521 AGSVARP 10 AGSVARP 10 AGSVARP 10 AGS AGSVARP 10 0.0004 X 108 AGSVARP 10 POL		16	절	688	ADATPTGWGLA	11		2058
POL 529 APPHOLMF 8 YOL 529 APPHOLMF 10 X 62 APSAGARA 9 X 62 APSAGARA 9 POL 655 APTRSPTY 9 POL 655 APTRSPTYA 9 POL 655 APTRSPTYA 10 POL 655 APTRSPTYA 10 POL 655 APTRSPTYA 11 POL 66 AGPCALFF 8 N 66 AGPCALFF 11 N 66 AGPCALFF 11 N AGPCALFF 11 0.0002 POL 521 AGPCALFF 11 POL 521 AGPCALFF 11 POL 521 AGPCALFF 9 NC 72 ALRFSAR 9 NC 73 ALRFSAR 9 NC 73 ALRFSAR 9 NC <		18	PQL	776	ADDPSRGR	co .		2059
POL 529 AFRHOLAFSY 10 X 62 AFSSAGPCA 9 X 62 AFSSAGPCA 9 X 62 AFTRSPTY 11 POL 655 AFTRSPTYKA 10 POL 655 AFTRSPTYKA 10 POL 655 AFTRSPTYKA 10 POL 656 AGPALLIR 8 ENV 180 AGPALLIR 8 X 66 AGPALLIR 8 POL 521 AGSWARAF 10 POL 521 ALNPADDPSR 10 POL 521 ALNPADDPSR 10 NC 41 ALREPHARA 9 POL 521 ALNPADDPSR 8 NA 41 ALNPADDPSR 8 NA 43 43 ENV 108 AANDWINSTITH 10 NA 43 ASALHVAWR 8 POL			POL	529	AFPHCLAF	œ		2060
X 62 AFSSAGPCALR 9 X 62 AFSSAGPCALR 11 POL 655 AFTESPTYK 9 0.2660 POL 655 AFTESPTYK 10 0.2660 POL 655 AFTESPTYK 11 0.2660 POL 655 AFTESPTYK 11 0.0004 FIN 160 AGPCALPF 11 0.0004 FOL 521 AGSVARRA 10 0.0002 POL 772 ALINPADDER 8 0.0003 X 70 ALRFTSAR 8 0.0004 K 102 AAGNOWISTITH 10 0.0004 FINA 108 AAGNOSSAR 8 0.0004 POL 690 AFFTSAR 8 0.0004 </td <td></td> <td>19</td> <td>PQL</td> <td>529</td> <td>AFPHCLAFSY</td> <td>10</td> <td></td> <td>2061</td>		19	PQL	529	AFPHCLAFSY	10		2061
X 62 AFSSAGPCALR 11 POL 655 AFTSPYY 9 POL 655 AFTSPTYKA 9 POL 655 AFTSPTYKAF 10 POL 655 AFTSPTYKAF 11 ENV 160 AGPCALRF 8 X 66 AGPCALRF 8 POL 521 AGCSVRRA 10 0.0002 POL 521 AGCSVRRA 10 0.0002 POL 521 AGCSVRRA 10 0.0003 POL 521 AGCSVRRA 10 0.0003 NAC 41 ALESPERGSH 11 0.0003 POL 521 AGCSVRRA 10 0.0003 X 70 ALESPERGSH 11 0.0003 X 102 AMOMNISTER 9 0.0004 NAC 34 ASALYRE 8 0.0003 POL 106 ASPCSSPY 8 0.00009		19	×	62	AFSSAGPCA	6		2062
POL 655 AFTRSPTY 8 POL 655 AFTRSPTYKA 10 0.2600 POL 655 AFTRSPTYKA 10 0.2600 POL 655 AFTRSPTYKA 10 0.0004 K 66 AGPCALBF 8 0.0004 X 66 AGPCALBF 11 0.0004 POL 18 AGPCALBF 10 0.0004 POL 521 AGPCALBF 10 0.0002 POL 521 AGPCALBF 10 0.0002 POL 521 AGENVRRAF 10 0.0002 POL 521 AGENVRRAF 10 0.0003 X 70 ALRTSAR 11 0.0003 X 70 ALRTSAR 9 0.0004 X 70 AMMINSTITH 10 0.0004 X ASPLHVANR 8 0.0004 POL 63 ASPLHVANR 9 0.0003 <tr< td=""><td></td><td>18</td><td>×</td><td>62</td><td>AFSSAGPCALR</td><td>11</td><td></td><td>2063</td></tr<>		18	×	62	AFSSAGPCALR	11		2063
POL 655 AFTESPTYK 9 0.2600 POL 655 AFTESPTYKAF 10 0.2600 POL 655 AFTESPTYKAF 11 0.2600 X 66 AGFLITR 8 0.0004 X 66 AGFLITRSA 11 0.0004 POL 521 AGENARTSA 10 0.0002 POL 521 AGENARAR 9 0.0002 POL 521 AGESVARA 9 0.0002 POL 521 AGESPHOSPH 10 0.0003 NC 772 ALINPODSRR 11 0.0003 X 70 ALRITSAR 8 0.0004 X 70 ALRITSAR 8 0.0004 X 102 AASALYREA 8 0.0004 POL 616 ASALYREA 8 0.0004 POL 620 AASALWARA 9 0.0009 X 63 CALRITSAR 9<		19	PQ	655	AFTESPTY	80		2064
POL 655 AFTESTYKA 10 POL 655 AFTESTYKAF 11 ENV 66 AGPCALIFT 8 X 66 AGPCALIFTSA 11 X 66 AGPCALIFTSA 11 POL 521 AGCSVARRA 9 -0.0002 POL 521 AGCSVARRA 10 -0.0002 POL 521 AGCSVARRA 10 -0.0002 POL 521 AGCSVARRA 10 -0.0002 POL 521 ALNPADDPSB 10 0.0003 X 70 ALNPADDPSB 10 0.0003 X 70 ALNPADDPSB 10 0.0003 X 102 AMOMNSTTFH 9 0.0003 X 102 AMOMNSTTFA 8 0.0004 NC 34 ASALYREA 8 0.0004 POL 822 ASPLHYAM 9 0.0009 X 69 CALAR		19	POL	655	AFTFSPTYK	თ	0.2600	2065
POL 655 AFTESPTYKAF 11 X 66 AGFCALFT 8 X 66 AGPCALFTSA 11 X 66 AGPCALFTSA 11 POL 18 AGPCALFTSA 11 POL 521 AGCSWARA 9 POL 521 AGCSWARA 9 POL 521 AGCSWARA 9 POL 521 ALNPADPSR 10 POL 772 ALNPADPSR 10 X 102 AMSTRAFAR 8 ENV 108 AMOWNSTTF 9 K 102 AMSTRAFAR 8 ENV 108 AMOWNSTTF 9 K 102 AMSTRAFAR 8 FOL 166 ASPLHVAWR 8 FOL 166 ASPLHVAWR 9 FOL 61 CAFSSAGPCA 10 X 69 CALFTSAR 8 CO		19	집	655	AFTFSPTYKA	10		2066
ENV 180 AGFILTR 8 X 66 AGPOLLFF 8 X 66 AGPOLLFTSA 11 X 6 AGPOLLFTSA 10 POL 521 AGSWARRA 9 POL 521 AGSWARRA 9 POL 521 AGSWARRA 10 POL 521 AGSWARRA 10 POL 772 ALNPADDPSR 10 K 7 ALRFTSAR 9 ENV 108 AMONNISTTF 9 K 102 AMONNISTTF 9 K 102 ASPLHVAWR 8 FOL 82 ASPLHVAWR 8 FOL 82 ASPLHVAWR 8 FOL		19	전	655	AFTFSPTYKAF	11		2067
X 66 AGPCALPF 8 X 66 AGPCALPFSA 11 0.0004 POL 18 AGPLEELPR 10 0.0002 POL 521 AGSWARA 9 0.0002 POL 521 AGSWARAF 10 0.0002 POL 72 ALNFADDPSR 10 0.0003 WC 71 ALNFADDPSR 10 0.0004 FNV 108 AMOMNSTIFF 9 0.0047 K 70 ALRFTSAR 8 0.0047 K 108 AMOMNSTIFF 9 0.0047 K 108 AMOMNSTIFF 9 0.0047 NC 34 ASPLHYAMR 8 0.0047 POL 166 ASPLHYAMR 9 0.0069 POL 61 CAASAGRA 9 0.0069 K 61 CAASAGRA 8 0.0009 X 69 CAASAGRA 9 0.0003 <		16	ENV	180	AGFFLTR	80		2068
X 66 AGPCALIFTSA 11 POL 18 AGPLEELPH 10 0.0004 POL 521 AICSWARA 9 -0.0002 POL 521 AICSWARAF 10 -0.0002 POL 521 AICSWARAF 10 0.0003 POL 772 ALMFTSAR 8 0.0003 K 70 ALMFTSAR 9 0.00047 ENV 108 AMONNISTIFH 9 0.00047 K 102 AMSITOLEA 9 0.00047 NLC 34 ASALYREA 8 0.00047 POL 166 ASFCGSPY 8 0.00047 POL 690 ATPTGWGLA 9 0.0009 FNV 84 ASTNRGSGP 9 0.0009 X 69 CALMFTSA 9 0.00034 X 69 CALMFTSAR 9 0.00034 X 6 COCOLUDPAR 9 0.0		18	×	99	AGPCALRF	80		2069
POL 18 AGPLEELPR 10 0.0004 POL 521 AGSWARA 8 -0.0002 POL 521 ALCSWARA 10 -0.0002 POL 521 ALCSWARA 10 -0.0002 NC 41 ALSPEHCSPH 10 0.0003 NC 41 ALSPEHCSPH 10 0.0004 K 70 ALRFISAR 8 0.0047 ENV 108 AMOWNSTTFH 10 0.00047 K 102 AMSITOLEA 8 0.0047 NLC 34 ASALYREA 8 0.0460 POL 166 ASTURGAS 8 0.0460 POL 822 ASTURGAS 8 0.0009 POL 690 ATPTGWGA 8 0.0009 X 69 CAARFITSAR 8 0.0003 X 69 CAARFITSAR 8 0.0003 X 6 COOLDPAR 9 <td></td> <td>18</td> <td>×</td> <td>99</td> <td>AGPCALRFTSA</td> <td>11</td> <td></td> <td>2070</td>		18	×	99	AGPCALRFTSA	11		2070
POL 521 AICSVVRR 8 -0.0002 POL 521 AICSVVRRA 9 -0.0002 POL 521 AICSVVRRAF 10 0.0003 NLC 41 ALESPEHCSPH 11 0.0003 POL 772 ALHPADPSR 9 0.0047 K 70 ALRTSAR 8 0.0047 ENV 108 AMONWISTIFH 10 0.0047 K 102 AMSTIDLEA 9 0.0460 NJC 34 ASALYREA 8 0.0460 POL 822 ASPLHVAWR 9 0.0060 POL 630 ATPTGWGLA 9 0.0060 FOL 650 CARWILR 8 0.0009 X 69 CALRFTSA 9 0.0034 X 69 CALRFTSA 9 0.0034 X 6 CALRFTSA 9 0.0034 X 6 CALRFTSAR 9		19	P'OL	18	AGPLEEELPR	10	0.0004	2071
POL 521 AICSWNRAA 9 POL 521 AICSWNRAAF 10 NLC 41 ALESPEHCSPH 11 POL 772 ALRATSAR 10 0.0003 X 70 ALRATSAR 8 0.0047 ENV 108 AMOWNSTTFH 10 0.0047 X 102 AMSTDLEA 9 0.0047 X 102 AMSTDLEA 9 0.0047 NUC 34 ASPLYAWR 8 0.0069 POL 66 ASPLYAWR 9 0.0069 POL 690 ATPTGWGLA 9 0.0009 FOL 690 ATPTGWGLA 9 0.0009 X 61 CAARSAGPCA 10 0.0009 X 69 CALRFISAR 9 0.00034 X 6 COCOLDPAR 9 0.00034 Y 6 COCOLDPAR 9 0.00034 X <		19	PQ	521	AICSWRR	80	-0.0002	2072
POL 521 AICSVVRRAF 10 NLC 41 ALESPEHCSPH 11 0.0003 POL 772 ALNPADDPSR 10 0.00047 K 70 ALRFTSAR 8 0.0047 ENV 108 AMOWNSTTFH 9 0.0047 K 102 AMSITDLEA 9 0.0047 NC 34 ASPLYREA 8 0.0460 POL 166 ASFLYREA 8 0.0460 POL 822 ASFLHVAWR 9 0.0009 POL 822 ASFLHVAWR 9 0.0009 POL 82 ASTNROSGR 9 0.0009 POL 755 CAANWILR 8 0.0009 X 61 CALRFISA 8 0.0004 X 69 CALRFISAR 9 0.0034 X 6 CCOLDPAR 9 0.0034 POL 723 GFAPSRSCA 9 0.0034 <td></td> <td>19</td> <td>PQ.</td> <td>521</td> <td>AICSVVRRA</td> <td>6</td> <td></td> <td>2073</td>		19	PQ.	521	AICSVVRRA	6		2073
NUC 41 ALESPEHCSPH 11 POL 772 ALNPADDPSR 10 0.0003 X 70 ALRFTSAR 8 0.00047 ENV 108 AMOWNISTTFH 10 0.00047 X 102 AMSTIDLEA 9 0.0046 X 102 ASALYREA 8 0.0460 POL 166 ASFCGSPY 8 0.0060 POL 822 ASPLHVAWR 9 0.0009 POL 822 ASPLHVAWR 9 0.0009 POL 630 ATPTGWGLA 9 0.0009 POL 630 ATPTGWGLA 8 0.0009 X 61 CALBFTSA 8 0.0003 X 69 CALBFTSA 8 0.0003 X 6 COCUDPAR 9 0.0003 POL 723 GFARSHSGA 9 0.0003		19	절	521	AICSVVRRAF	10		2074
POL 772 ALNPADDPSR 10 0.0003 X 70 ALRFTSAR 8 0.0047 ENV 108 AMOWNSTTF 10 0.0047 X 102 AMSTDLEA 9 0.00460 X 102 AMSTDLEA 8 0.0460 POL 166 ASPCGSPY 8 0.0460 POL 822 ASPLHVAWR 9 0.0009 POL 690 ATPTGWGLA 9 0.0009 POL 755 CAANWILR 8 0.0009 X 69 CALRFTSA 8 0.00034 X 6 CCALDPAR 9 0.00034 POL 723 GFARSGA 9 0.00034		19	MC	41	ALESPEHCSPH	11		2075
X 70 ALRFTSAR 8 0.0047 ENV 108 AMOWNSTTFH 10 10 ENV 108 AMOWNSTTFH 10 10 X 102 AMSITDLEA 9 0.0460 NLC 34 ASALYREA 8 0.0460 POL 166 ASPLHVAWR 9 0.0009 FOL 84 ASTNROSGR 9 0.0009 FOL 690 ATPTGWGLA 9 0.0009 FOL 755 CAANWILR 8 0.0009 X 61 CAERFTSAR 8 0.0003 X 69 CALRFTSAR 9 0.0034 X 6 CCOLDPAR 8 0.0034 POL 723 GFARSRSA 9 0.0034		18	전	772	ALNPADDPSR	10	0.0003	2076
ENV 108 AMOWNSTTFH 9 KL 108 AMOWNSTTFH 10 NLC 34 ASALYREA 9 NLC 34 ASPCGSPY 8 POL 166 ASPCGSPY 8 0.0460 POL 822 ASPLHVAWR 9 0.0009 FOL 690 ATPTGWGLA 9 0.0009 POL 755 CAANWILR 8 0.0009 X 61 CAFSSAGPCA 10 8 X 69 CALRFTSA 8 0.0034 X 69 CALRFTSAR 8 0.0034 Y 6 COOLDPAR 9 0.0034 POL 723 CFARSRSGA 9 0.0034		17	×	70	ALRFTSAR	60	0.0047	2077
ENV 108 AMOWNSTTFH 10 X 102 AMSITDLEA 9 NLC 34 ASALYREA 9 POL 166 ASFOGSPY 8 0.0460 POL 822 ASPLHVAWR 9 0.0009 ENV 84 ASTNROSGR 9 0.0009 POL 755 CAANWILR 8 0.0009 X 61 CAFSSAGPCA 10 0.0034 X 69 CALRFTSA 8 0.0034 X 6 CCALPPAR 8 0.0034 POL 723 GFARSRSGA 9 0.0034		16	EN	108	AMOWNSTTF	6		2078
X 102 AMSITDLEA 9 NUC 34 ASALYREA 8 0.0460 POL 166 ASPCGSPY 8 0.0460 POL 822 ASPLHVAWR 9 0.0009 ENV 84 ASTINROSGR 9 0.0009 POL 755 CAANWILR 8 0.0009 X 69 CALRFTSA 8 0.0034 X 6 CCALRFTSAR 8 0.0034 POL 723 CFARSRSGA 9 0.0034		16	ENA	108	AMOWNSTTFH	10		2079
NUC 34 ASALYREA 8 0.0460 POL 166 ASPCGSPY 8 0.0460 POL 822 ASPLHVAWR 9 0.0009 ENV 84 ASTNROSGR 9 0.0009 POL 690 ATPTGWGLA 8 0.0009 POL 755 CAANWILR 8 0.0034 X 69 CALRFTSA 8 0.0034 X 6 CCALPTSAR 9 0.0034 POL 723 CFARSRSGA 9 0.0034		15	×	102	AMSITDLEA	6		2080
POL 166 ASFCGSPY 8 0.0460 POL 822 ASPLHVAWR 9 0.0460 ENV 84 ASTNROSGR 9 0.0009 POL 690 ATPTGWGLA 9 0.0009 POL 755 CAANWILR 8 0.0009 X 69 CALRFTSA 8 0.0034 X 6 CCALRFTSAR 9 0.0034 POL 723 CFARSTSGA 9 0.0034		17	SEC	34	ASALYREA	80		2081
POL 822 ASPLHVAWR 9 ENV 84 ASTNROSGR 9 0.0009 POL 690 ATPTGWGLA 9 0.0009 POL 755 CAANWILR 8 10 X 61 CALRFTSA 8 0.0034 X 69 CALRFTSAR 9 0.0034 POL 723 CFARSRSGA 9		20	전	166	ASFCGSPY	80	0.0460	2082
ENV 84 ASTNROSGR 9 0.0009 POL 690 ATPTGWGLA 9 0.0009 POL 755 CAANWILR 8 10 X 69 CALRFTSA 8 0.0034 X 69 CALRFTSARR 9 0.0034 POL 723 CFARSRSGA 9 9		16	전	822	ASPLHVAWR	6		2083
POL 690 ATPTGWGLA 9 POL 755 CAANWILR 8 X 61 CAERSAGPCA 10 X 69 CALRETSAR 9 0.0034 X 6 CCOLDPAR 8 0.0034 POL 723 CFARSRSGA 9		15	EN	84	ASTNROSGR	6	0.0009	2084
755 CAANWILR 8 61 CAESSAGPCA 10 69 CALRFTSA 8 69 CALRFTSAR 9 6 OCOLDPAR 8 723 CFARSRSGA 9		16	전	069	ATPTGWGLA	6		2085
61 CAFSSAGPCA 10 69 CALRFTSA 8 69 CALRFTSAR 9 0.0034 6 CCOLDPAR 8 723 CFARSRSGA 9		16	PQ.	755	CAANWILR	60		2086
69 CALRFTSA 8 69 CALRFTSAR 9 0.0034 6 CCOLDPAR 8 723 CFARSRSGA 9		19	×	61	CAFSSAGPCA	10		2087
69 CALRFTSAR 9 0.0034 6 CCQLDPAR 8 723 CFARSRSGA 9		18	×	. 69	CALRFTSA	8		2088
6 CCQLDPAR 723 CFARSRSGA 9		17	×	69	CALRETSAR	6	0.0034	2089
723 CFARSRSGA 9		16	×	9	CCQLDPAR	œ		2090
		17	PQ.	723	CFARSRSGA	6		2091

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Conservancy	Freq.	Protein	Position	Sequence	АА	A'0301	SeqID Num.
75	15	PQ.	607	CFBKLPVNR	o		2092
95	19	집	638	CGYPALMPLY	. 0		2093
95	19	POL	638	CGYPALMPLYA	=		2094
100	20	ENV	312	CIPIPSSWA	6		2095
100	20	ENV	312	CIPIPSSWAF	10		2096
80	16	EVN	312	CIPIPSSWAFA	11		2097
95	19	EN	253	CLIFLLVLLDY	11	0.0083	2098
06	18	×	17	CLRPVGAESR	10	0.0011	2099
95	19	ENV	239	CLARFIF	8		2100
75	15	ENV	239	CLARFIIRE	10		2101
100	20	SEC S	48	CSPHHTALR	6	0.0029	2102
100	20	SPC SPC	48	CSPHHTALRQA	=		2103
95	19	POL	523	CSWRRAF	8		2104
95	19	전	523	CSWRRAFPH	10		2105
100	20	EN	310	CTCIPIPSSWA	=		2106
80	16	PQ.	689	DATPTGWGLA	10		2107
06	18	정	540	DDVVLGAK	80		2108
06	18	SE SE	31	DIDPYKEF	8		2109
06	18	NC NC	31	DIDPYKEFGA .	10		2110
85	17	NC NC	29	DLLDTASA	89		2111
85	17	SEC SEC	29	DLLDTASALY		0.0001	2112
85	17	NC NC	59	DLLDTASALYR		0.0042	2113
95	19	ENV	196	DSWMTSLNF		9000.0	2114
85	17	SEC C	32	DTASALYR	8	0.0004	2115
80	16	2	32	DTASALYREA	10		2116
95	19	×	14	DVLCLRPVGA	10		2117
95	19	전	418	DVSAAFYH	8		2118
06	18	전	541	DVVLGAKSVQH			2119
92	19	절	17	EAGPLEEELPR	-	-0.000	2120
06	18	3	40	EALESPEH	8		2121
06	18	집	718	ELLAACFA	8		2122
06	18	절	718	ELLAACFAR	6	0.0002	2123
. 85	17	POL	718	ELLAACFARSR	=	0.0082	2124
92	19	25	. 43	ELLSFLPSDF	10		2125
95	19	2	43	ELLSFLPSDFF			2126
95	19	2	43	ESPEHCSPH	6		2127
95	19	3	43	ESPEHCSPHH	10		2128
92	19	전	374	ESRLVVDF	8		2129
95	19	<u>S</u>	374	ESRLWDFSQF	=		2130
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Table XVI HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
95	19	2	174	ETTWRRR	80	0.0003	2131
80	16	NC	174	ETTWARRGR	10	0.0003	2132
95	19	PQ.	631	FAAPFTQCGY	10		2133
85	17	PO	724	FARSRSGA	80		2134
80	16	PQ.	821	FASPLHVA	80		2135
80	16	전	821	FASPLHVAWR	10		2136
06	18	EN	13	FFPDHQLDPA	. 10		2137
85	17	EN	13	FFPDHQLDPAF			2138
75	15	SEC	139	FGRETVLEY	o		2139
75	15	전	244	FGVEPSGSGH	10		2140
95	19	2	122	FGVWIRTPPA	10		2141
95	19	SEC	122	FGVWIRTPPAY	=		2142
80	16	EN<	248	FILLOLIF	o		2143
80	16	EN	246	FLFILLLCLIF			2144
75	15	EN	171	FLGPLLVLQA	10		2145
95	19	<u>5</u>	513	FLLAQFTSA	6	90000	2146
95	19	<u>5</u>	562	FLLSLGIH	89		2147
95	19	EN	256	FLLVLLDY	8	0.0050	2148
100	20	전	363	FLVDKNPH	80		2149
92		Pol	658	FSPTYKAF	8		2150
95	19	×	. 69	FSSAGPCA	80		2151
06	18	×	63	FSSAGPCALR	10		2152
06	18	×	63	FSSAGPCALRF	11		2153
100	20	EN	333	FSWLSLLVPF	10	0.0004	2154
06	18	PQ.	536	FSYMDDVVLGA	=		2155
95	19	전	959	FIFSPIYK	8	0.0100	2156
95	19	PQ.	656	FTFSPTYKA	6		2157
95	19	Pol	656	FIFSPTYKAF	10	0.0004	2158
95	19	Po	635	FTOCGYPA	œ		2159
95	19	절	518	FTSAICSVVR	10	0.0003	2160
95	19	전	518	FTSAICSWRR		0.0065	2161
95	19	×	132	FWLGGCRH	80		2162
06	2	×	132	FVLGGCRHK	თ	0.0430	2163
06	18	전	. 992	FVYVPSALNPA	11		2164
80	16	절	754	GCAANWILR	6		2165
95	19	전	630	GFAAPFTOOGY	11		2166
06	18	EN	12	GFFPDHOLDPA	11		2167
75	15	EN	170	GFLGPLLVLOA	11		2168
85	17	EN	61	GGLLGWSPQA	10		2169

Table XVI HBV A03 Motif With Binding

				HBV AUS MOTIT WITH BINGING		•	
Conservancy	Freq.	Protein	Position	Sequence	АА	A'0301	SeqID Num
100	20	Į od	360	SIGN HVDR	œ		2170
100	20	ā	360	HANXUN HAUST	÷ -		2171
75	15	걸	567	GIFLUPUK	. co		2172
75	15	Pol	267	GIHLNPNKTK	10	0.0025	2173
75	15	POL	267	GIHLNPNKTKR	11		2174
85	17	<u>R</u>	682	GLCQVFADA	თ	0.0001	2175
95	19	<u>P</u>	627	GLIGFAAPF	б	9000.0	2176
85	17	ENV	62	GLIGWSPOA	6		2177
95	19	×	57	GLPVCAFSSA	10		2178
98	19	<u>5</u>	509	GLSPFLLA			2179
95	19	Po	509	GLSPFLLAGF	10	•	2180
85	17	NC	29	GMDIDPYK	8	9000.0	2181
85	17	NC S	29	GMDIDPYKEF	10	-0.0003	2182
06	18	전	735	GTDNSVVLSR	10	0.0010	2183
90	18	전	735	GTDNSVVLSRK	-	0.0140	2184
80	16	Pol	763	GTSFVYVPSA	10		2185
80	16	전	245	GVEPSGSGH	o		2186
100	20	POL	361	GVFLVDKNPH	10		2187
80	16	PQ.	207	GVGLSPFLLA	10		2188
95	19	NC NC	123	GWWIRTPPA	O		2189
98	19	SEC SEC	123	GVWIRTPPAY	10	0.0047	2190
95	19	SEC SEC	123	GWWIRTPPAYR	Į.	0.1900	2191
100	20	SPC SPC	47	HCSPHHTA	. 80		2192
100	20	SPC	47	HCSPHHTALR	10		2193
80	16	PQ.	820	HFASPLHVA	6		2194
80	16	POL	820	HFASPLHVAWR	11		2195
. 56	19	×	49	HGAHLSLR	89		2196
85	17	ENS	09	HGGLLGWSPQA	11		2197
06	18	SEC.	104	HISOLTEGR	6		2198
75	15	전	569	HLNPNKTK	σο		2199
75	15	전	• 695	HLNPNKTKR	6		2200
06	18	×	52	HLSLRGLPVCA	11		2201
80	16	짇	491	HLYSHPIILGF			2202
85	17	Z Z	715	HTAELLAA	80		2203
85	17	전	715	HTAELLAACF	10		2204
85	17	PQ.	715	HTAELLAACFA			2205
100	20	전	149	HTLWKAGILY	10	0.0440	2206
100	20	집	149	HTLWKAGILYK	11	0.5400	2207
95	19	ğ Z	522	ICSWARA	80		2208
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Table XVI HBV A03 Motif With Binding.

				HBV AUS MOTH WITH BINGING			
Conservancy Freq.	Freq.	Protein	Position	Sequence	АА	A'0301	SeqID Num
95	19	Ö	522	ICSWARAF	o		6066
95	6	집	522	ICSVVRRAFPH	. =		2210
06	8	NC NC	32	IDPYKEFGA	்		2211
06	18	POL	617	IDWKVCQR	80		2212
100	20	EN	381	IFFCLWVY	80		2213
95	19	EN	255	IFLLVLLDY	o		2214
80	16	PO	734	IGTDNSVVLSR	. 11		2215
100	20	EN	249	ILLICUF	89		2216
80	16	PO	760	ILRGTSFVY	თ	0.0440	2217
90	18	<u>N</u>	105	ISOLTFGR	8	0.0004	2218
06	18	전	625	IVGLLGFA	89		2219
06	. 8	<u>S</u>	625	IVGLLGFAA	o		2220
90	18	POL.	625	IVGLLGFAAPF	11		2221
100	50	Po	153	KAGILYKR	8	0.0002	2222
80	16	Ą	503	KIPMGVGLSPF	11		2223
75	15	ᅙ	108	KLIMPARF	89		2224
75	15	<u>0</u>	108	KLIMPARFY	6		2225
80	16	전	610	KLPVNRPIDWK	#		2226
85	17	<u>P</u>	574	KTKRWGYSLNF	1		2227
75	15	×	130	KVFVLGGCR	6	0.0420	2228
75	15	×	130	KVFVLGGCRH	10		2229
95	9	전	55	KVGNFTGLY	6	0.2100	2230
85	17	전	720	LAACFARSR	6	0.0058	2231
95	19	×	16	LCLRPVGA	80		2232
06	18	×	16	LCLRPVGAESR	11.		2233
95	19	PQ.	683	LCOVFADA	80		2234
100	50	PQ	125	LDKGIKPY	80		2235
100	20	진	125	LDKGIKPYY	6		2236
80	16	×	б	LDPARDVLCLR	-1		2237
95	19	ENC	195	LDSWWTSLNF	10		2238
85	17	STC C	31	LDTASALY	80	-	2239
85	17	STC C	31	LDTASALYR	O	0.0004	2240
80	16	SPC	31	LDTASALYREA	11		2241
95	19	Z Z	417	LDVSAAFY	8		2242
95	19	ರ್	417	LDVSAAFYH	6		2243
80	16	EN	247	. FILLLOLIF	10		2244
92	19	진	544	LGAKSVQH	80		2245
80	16	절	753	LGCAANWILR	10		2246
75	15	전	266	LGIHLNPNK	o		2247

Table XVI HBV A03 Motif With Binding

				HBV AUS MOTIF WITH BINGING			
Conservancy Freq.	Freq.	Protein	Position	Sequence		A'0301 S	SeqID Num
75	15	<u>5</u>	566	LGIHLNPNKTK	-		2248
95	19	EN	172	LGPLLVLQA	6		2249
95	19	EN	172	LGPLLVLQAGF			2250
95	19	₩	254	LIFLLVLLDY	10	0.0022	2251
100	20	POL	109	LIMPARFY	8	-0.0002	2252
90	18	전	719	LLAACFAR	8	0.0024	2253
85	17	Po Po	719	LLAACFARSR	. 10		2254
95	. 61	전	514	LLAQFTSA	8		2255
85	17	NC	30	LLDTASALY	6	0.0013	2256
85	17	SP	30	LLDTASALYR	10	0.0050	2257
80	16	<u>5</u>	752	LLGCAANWILR	=		2258
95	19	전	628	LLGFAAPF	8		2259
85	17	™	63	LLGWSPQA	- α		2260
100	20	ETV	378	LLPIFFCLWVY	1	0.0230	2261
95	19	S C	44	LLSFLPSDF	6		2262
95	19	NC	44	LLSFLPSDFF	10		2263
95	19	EN	175	LLVLQAGF	8		2264
95	19	EN	175	LLVLQAGFF	6	9000.0	2265
100	20	EN	336	LLVPFVQWF	6		2266
85	17	SEC	100	LLWFHISCLTF	==		2267
95	19	NC	45	LSFLPSDF	88		2268
95	19	ST.	45	LSFLPSDFF	6	9000.0	2269
95	19	Pol	415	LSLDVSAA	8		2270
98	19	PQ.	415	LSLDVSAAF	6	0.0004	2271
95	19	Po	415	LSLDVSAAFY	10		2272
95	19	PQ	415	LSLDVSAAFYII			2273
75	15	절	564	LS:LG!HLNPNK	=	٠	2274
100	20	ENS	336	LSLLVPFVQWF	=		2275
95	19	×	53	LSLRGLPVCA	10		2276
95	19	×	53	LSLRGLPVCAF	=		2277
95	19	PQ.	510	LSPFLLAQF	6		2278
9 5 85	17	전	742	LSRKYTSF	8		2279
95	19	NC	169	LSTLPETTVVR	=	-0.0009	2280
75	15	EN		LSVPNPLGF	6		2281
100	20	전	412	LSWLSLDVSA	10	0.0048	2282
100	19	PO	412	LSWLSLDVSAA	11		2283
95	15	전	8	LSYQIIFRK	80		2284
75	15	ST.	137	LTFGRETVLEY	1		2285
85	17	POL	66	LTVNEKRR	89	-0.0002	2286

Table XVI HBV A03 Motif With Binding

Conservancy Freq.	Freq.	Protein	Position	Sequence	AA	A'0301 S	SeqID Num
95	19	ENS	176	LVLOAGFF	œ		2287
100	20	EN	339	LVPFVQWF	. 80	0.0028	2288
06	18	NC	119	LVSFGVWIR	6		2289
100	20	POL	377	LWDFSQF	8	0.0016	2290
100	20	PQ.	377	LWDFSQFSR	10		2291
95	19	EN	238	MCLARFIIF	6		2292
75	15	EN	238	MOLARFIIFLE	. 11		2293
06	18	전	539	MDDWLGA	8		2294
06	18	POL	539	MDDWLGAK	თ		2295
06	18	SPC	30	MDIDPYKEF	o		2296
06	18	200	30	MDIDPYKEFGA	11		2297
80	16	전	506	MGVGLSPF	8		2298
80	16	PO	506	MGVGLSPFLLA	11		2299
85	17	EN	360	MMWYWGPSLY	10	0.0500	2300
80	16	×	103	MSTTDLEA	8		2301
75	15	×	103	MSTTDLEAY	6	0.0008	2302
75	15	×	103	MSTTDLEAYF	10		2303
75	15	×	103	MSTTDLEAYFK	-		2304
95	19	PQ	561	NFLLSLGIH	0		2305
06	18	NC	75	NLEDPASR	80	-0.0002	2306
95	19	절	45	NLNVSiPWTH	10		2307
95	19	PQ.	45	NLNVSIPWTHK	=	-0.0009	2308
95	15	EN	15	NLSVPNPLGF	10		2309
06	18	POL	411	NLSWLSLDVSA			2310
75	15	EN	215	NSOSPTSNH	6		2311
06	18	Po	738	NSVVLSRK	88	9000.0	2312
06	18	Po	738	NSVVLSRKY	o	0.0020	2313
100	20	절	47	NVSIPWTH	80		2314
100	20	전	47	NVSIPWTHK	6	0.0820	2315
06	18	절	775	PADDPSRGR	O	0.0008	2316
95	19	PQ.	641	PALMPLYA	8		2317
75	15	×	145	PAPCNFFTSA	10		2318
80	16	×	=	PARDVLCLR	6	0.0002	2319
06	18	전	355	PARVTGGVF	6		2320
75	15	EN	83	PASTNROSGR	10		2321
95	19	SEC SEC	130	PAYRPPNA	80		2322
06	18	×	89	PCALRFTSA	6		2323
85	17	×	89	PCALRFTSAR	10		2324
75	15	×	147	PCNFFTSA	8		2325

Table XVI HBV A03 Motif With Binding.

				HEV AUS MOUIT WILL BINGING			
Conservancy	Freq.	Protein	Position	Sequence	АА	A'0301 S	SeqID Num
20	9	NA NA	Ť.	₹aci OHca	α		9396
2 6	2 2		2 1				2020
. 96	ο c	<u> </u>	15	רטדונים סבי - אסבורא	, c		2327
5 0	n C	<u> </u>	2.0		2 6		2350
	n (223		n c	8000	2220
00 S	07	N W	233	PSYBAMAC BB	, C	0.0008	2331
92	19	ENS	233	PGYRWMOLRAF	-		2332
06	18	Pol	616	PIDWKVCQR	်က	0.0002	2333
100	20	ENV	380	PIFFCLWVY	o	0.0011	2334
85	17	POL	713	PIHTAELLA	6		2335
. 85	17	<u>S</u>	713	PIHTAELLAA	10		2336
80	16	Pol	496	PILGFRK	8		2337
100	20	EN	314	PIPSSWAF	80		2338
80	16	ENV	314	PIPSSWAFA	6		2339
100	20	PQ.	124	PLDKGIKPY	6	0.0001	2340
100	20	전	124	PLDKGIKPYY	10	0.0002	2341
95	19	전	20	PLEEELPR	88	0.0002	2342
06	16	PQ.	20	PLEEELPRLA	10		2343
06	19	EN	10	PLGFFPDH	8		2344
100	20	PQ.	427	РГНРААМРН	6	0.0012	2345
95	19	EN	174	PLLVLQAGF	O		2346
95	19	ENS	174	PLLVLQAGFF	10		2347
80	16	정	711	PLPIHTAELLA	11		2348
100	20	POL	2	PLSYQHFR	80	-0.0002	2349
75	15	PQ.	2	PLSYQHFRK	6	0.0011	2350
85	17	PQ.	86	PLTVNEKR	8	0.0002	2351
85	17	전	86	PLTVNEKRR	თ	0.0008	2352
80	16	PQ.	505	PMGVGLSPF	O		2353
85	17	전	797	PTTGRTSLY	0	0.0001	2354
85	17	정	197	PTTGRTSLYA			2355
95	19	×	29	PVCAFSSA	∞		2356
06	18	×	20	PVGAESRGR	0	0.0002	2357
85	17	전	612	PVNRPIDWK	6	0.0310	2358
95	19	절	654	QAFTFSPTY ·	6	0.0030	2359
95	19	집	654	QAFTFSPTYK	10	0.0450	2360
95	19	집	654	QAFTFSPTYKA			2361
80	16	EN	179	QAGFFLTR	ი		2362
80	16	ENS	107	QAMQWNSTTF	10		2363
80	16	EN	107	QAMQWNSTTFH	₹		2364

Table XVI HBV A03 Motif With Binding.

				HBV A03 Motif With Binding			
Conservancy Freq.	Freq.	Protein	Position	Sequence	АА	A'0301 Sec	SeqID Num
95	19	전	637	QCGYPALMPLY	11		2365
95	19	절	517	QFTSAICSVVR	=		2366
75	15	SEC SEC	169	CSPRARRSOSR			2367
80	16	Pol	189	OSSGILSR	8		2368
95	19	Pol	528	RAFPHCLA	8		2369
95	19	Ē	528	RAFPHCLAF	6	0.0015	2370
95	19	정	528	RAFPHCIAFSY	. 11	0.1200	2371
85		SEC SEC	28	RDLLDTASA	თ		2372
. 82	17	ST.	28	RDLLDTASALY	11		2373
95	19	×	13	RDVLCLRPVGA	11		2374
100	20	ENA	332	RFSWLSLLVPF	11		2375
95	19	×	56	RGLPVCAF	8		2376
95	19	×	56	· PGLPVCAFSSA			2377
100	20	NC	152	RGASPARA	8		2378
80	16	전	762	RGTSFVVVPSA	-11		2379
06	18	<u>S</u>	624	PNGLLGF .	80		2380
06	18	PQ.	624	RIVGLLGFA	6		2381
06	18	PQ.	624	RIVGLLGFAA	10		2382
75	15	<u>S</u>	106	RLKLIMPA	ω	٠	2383
75	15	PQ.	106	RLKLIMPAR	o	0.0950	2384
75	15	전	106	RLKLIMPARF	10		2385
75	15	Pol	106	RLKLIMPARFY	11		2386
75	15	×	128	RLKVFVLGGCR	11		2387
95	19	POL	376	RLVVDFSQF	o	9000.0	2388
95	19	전	376	RLVVDFSQFSR	11	0.2800	2389
95	19	NC	163	RSPRRITPSPR	11	-0.0007	2390
75	15	STC STC	167	RSOSPARR	8		2391
75	15	SEC SEC	167	RSQSPRPR	o		2392
90	18	POL	353	RTPARVTGGVF	11		2393
98	19	ST ST ST ST ST ST ST ST ST ST ST ST ST S	127	. RTPPAYRPPNA	11		2394
95	19	SEC SEC	188	, RTPSPRPR	89	-0.0002	2395
95	19	NC NC	188	RIPSPRARR	o	0.0054	2396
95	16	POL	818	RVHFASPLH	6		2397
75	15	POL	818	RVHFASPLHVA	11		2398
100	20	<u>o</u>	357	RVTGGVFIVDK	-	0.0190	2399
06	18	×	65	SAGPCALR	89	-0.0002	2400
90	18	×	65	SAGPCALRF	O	-0.0003	2401
95	19	PQ.	520	SAICSVVR	8	-0.0002	2405
95	19	POL	520	SAICSVVAR	6	0.0058	2403

Table XVI HBV A03 Motif With Binding

				HEV AUS MOTH WITH BINGING			
Conservancy Freq.	Freq.	Protein	Position	Sequence	АА	A'0301	SeqID Num
	4	Š					
ຄ	<u>.</u>	<u></u>	220	SAICSWHHA	91		2404
95	19	PQ.	520	SAICSWRRAF			2405
95	18	절	171	SALNPADDPSR	11	-0.0004	2406
06	20	2	165	SASFCGSPY	6		2407
100	18	SEC	121	SFGVWIRTPPA	11		2408
06	19	NC S	46	SFLPSOFF	8		2409
95	15	PO	748	SFPWLIGCA	6		2410
75	15	POL	740	SFPWLLGCAA	10		2411
75	16	PQ.	765	SFVWPSA	8		2412
80	20	POL	49	SIPWTHKVGNF	11		2413
100	19	ENV	194	SLDSWMTSINF	11		2414
95	19	전	416	SLDVSAAF	8		2415
95	19	POL	416	SIQVSAAFY	. 6	0.0016	2416
95	19	POL	416	SLDVSAAFYH	10		2417
75	15	PQ.	565	SIGIHLNPNK	10		2418
100	20	EN	337	SLLVPFVQWF	10		2419
95	19	×	54	SLRGLPVCA	6		2420
95	19	×	54	SLRGLPVCAF	10	0.0004	2421
95	18	×	64	SSAGPCALR	6	0.0080	2422
06	18	×	64	SSAGPCALRF		-0.0003	2423
06	19	SEC.	170	STIPETTVVR	10	0.0007	2424
95	19	SE SE	170	STLPETTWRR	1	0.0150	2425
95	16	ENV	85	STNROSGR	8		2426
. 08	15	×	104	STTDLEAY	8		2427
75	15	×	104	STTDLEAYF	6		2428
75	15	×	104	~		9900'0	2429
75	15	ENV	17	SVPNPLGF	8		2430
06	8	전	739	SVVLSHKY	ಐ	-0.0002	2431
85	17	POL	739	SVVLSRKYTSF	11		2432
95	19	Po	524	SWRRAFPH	6	0.1100	2433
85	17	Pol	716	TAELLAACF	6		2434
85	17	전	716		10		2435
85	17	Pol	716	TAELLAACFAR	11	9000.0	2436
80	16	SC		TASALYREA	6		2437
100	20	ENA	311	TCIPIPSSWA	10		2438
100	20	ENS	311	TCIPIPSSWAF	11		2439
80	16	×	106	TDLEAYFK	8		2440
06	18	ᅙ.	736	TDNSVVLSR	6		2441
06	18	Pol	, 736	TDNSVVLSRK	10	9000.0	2442
			-				

Table XVI HBV A03 Motif With Binding

Sequence

Position

Protein

Conservancy Freq.

SeqID Num

A'0301

AA

	2442	2442	2444	2446	2447	2448	2449	2450	2451	2452	2453	2454	2455	2456	2457	2458	2459	2460	2461	2462	2463	2464	2465	2466	2467	2468	2469	2470	2471	2472	2473	2474	2475	2476	2477	2478	2479	2480	2481
The second secon					0.0007		0.0008	0.0007	0.0005	0.1300	5.3000	0.0082	0.0005	0.0018						9000.0	0.0004			0.0008	0.0003														
			2 0	ာတ	o	9	6.	10	=	6	10	=	6	10	11	10		6	8	6	80	6	89	6	89	=			89	6	æ	ę.	10	æ	æ	10	6	1	8
	VAGS RASHGE	TECRETA EV	TESPTOKA	TESPTYKAF	TGGVFLVQK	TGRTSLYA	TLPETTVVR	TLPETTWAR	TLPETTVVRRA	TLWKAGILY	TLWKAGILYK	TLWKAGILYKR	TSAICSVVR	TSAICSWAR	TSAICSVVRRA	TSFPWLLGCA	TSFPWLLGCAA	TSFVYVPSA	TTDLEAYF	TTDLEAYFK	TTGRTSLY	TTGRTSLYA	TISTGPCK	TTVVRRRGR	TVVRARGA	TWARRGRSPR	VCAFSSAGPCA	VOORNGLLGF	VDFSQFSR	VFLVDKNPH	VFVLGGCR	VFVLGGCRH	VFVLGGCRHK	VGAESRGR	VGLLGFAA	VGLLGFAAPF	VGLSPFLLA	VGLSPFLLAQF	VGNFTGLY
	201	130	130	857	359	1 662	171	171	171	150	150	150	519	519	519	747	747	764	105	105	198	798	278	175	176	176	09	621	379	362	131	131	131		979	979	. 508	508	- 26
	ā	Z <u>z</u>	3 €	ಕ್ಷ ಕೃ	절	징	SE SE	3	SE	전	전	전	ᅙ	ᅙ	짇	전	PO	Pol	×	×	Po	집	EN	SK K	NC	SEC NEC	×	절	PQ.	절	×	×	×	×	절	Z Z	PO	PO	Po[-
	ç	o 4	2 5	. .	20	17	19	19	19	20	20	20	19	19	19	15	15	16	15	15	17	17	15	16	16	16	19	17	20	20	16	16	15	19	19	19	16	16	19
	o o	30		0.00	100	85	95	95	95	100	100	100	95	95	95	75	75	80	75	75	85	85	75	80	80	80	92	85	100	100	80	80	75	92	92	95	80	80	92

Table XVI HBV A03 Motif With Binding

Conservancy	Freq.	Protein	Position	Sequence	АА	A'0301	SeqID Num
							Ī
85	17	Po	96	VGPLTVNEK	6	0.0007	2482
85	17	PQ.	96	VGPLTVNEKR	10		2483
85	17	POL	96	VGPLTVNEKRR	==		2484
95	19	×	15	VLCLRPVGA	6		2485
95	19	POL	543	VLGAKSVQH	6		2486
90	18	×	133	M.GGCRHK	8	0.0150	2487
80	16	ENA	177	VLQAGFFLLTR	=		2488
85	17	<u>R</u>	741	VLSRKYTSF	0		2489
90	18	SEC SEC	120	VSFGVWIR	8	0.0040	2490
100	20	POL	48	VSIPWTHK	8	0.0130	2491
100	20	<u>S</u>	358	VTGGVFLVDK	10	0.0390	2492
100	20	<u>R</u>	378	WDFSQFSR	6	0.0015	2493
06	18	POL	542	VVLGAKSVQH	10		2494
85	17	<u>R</u>	740	VVLSRKYTSF	10	0.0004	2495
95	19	PQ	525	VVRBAFPH	8		2496
95	19	Pol	525	WRRAFPHCLA	11		2497
80	16	NC	177	WARAGASPA	10	0.0027	2498
80	16	NC	177	WARRGRSPAR			2499
06	18	N.C.	102	WFHISCLTF	6	•	2500
90	16	SE SE	102	WFHISOLTFGR	11		2501
85	17	SEC PEC	28	WGMDIDPY	8		2502
85	17	SEC SEC	28	WGMDIDPYK	6	-0.0003	2503
85	17	SEC SEC	28	WGMDIDPYKEF	-1		2504
85	17	Pol	578	WGYSLNFMGY	10		2505
80	16	<u>7</u> 0	759	WILBGTSF	. 8		2506
80	16	PQ.	759	WILRGTSFVY	10	0.0076	2507
95	19	SHC SHC	125	WIRTPPAY	8	-0.0002	2508
98	19	ž	125	WIRTPPAYR	6	0.0008	2509
06	18	정	314	WLQFRNSK	8	-0.0002	2510
100	20	<u>Б</u>	414	WLSLDVSA	89		2511
95	19	전	414	WLSLDVSAA	6		2512
95	19	전	414	WLSLDVSAAF	10		2513
95	19	집	414	WLSLDVSAAFY		0.0034	2514
. 100	20	EN	335	WLSLLVPF	8		2515
85	17	5	26	WLWGMDIDPY	10	0.0002	2516
85	17	S C	26	WLWGMDIDPYK		0.0030	2517
95	19	ENA	237	WMCLRRFIIF	10	0.0004	2518
85	17	EN		WMMMYWGPSLY		0.000	2519
100	20	<u>Ö</u>	52	WTHKVGNF	8		2520

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Table	Motif
	A03
	HBV

				TEV AUS WOTH WITH BINGING			
Conservancy	Freq.	Protein	Position	Sequence	АА	A'0301 S	SeqID Num
100	20	POL		YLHTLWKA	8		2521
100	20	정	122	YLPLDKGIK	o	0.0001	2522
100	20	POL		YLPLDKGIKPY		-0.0004	2523
06	18	2		YLVSFGVWIR	10	0.0005	2524
06	18	PO		YMDDVVLGA		0.0001	2525
06	18	PQ.		YMDDWLGAK	10	0.0330	2526
80	16	PQ		YSHPIILGF	o		2527
80	16	互		YSHPIILGFR	10		2528
80	16	P2		YSHIPIILGFRK	11		2529
85	17	PQL		YSLNFMGY	8	-0.0002	2530
75	15	Ю		YTSFPWLLGCA	11		2531
06	18	전		YVPSALNPA	6		2532

Table XVII A11 Motif With Binding Information

			<u>-</u> *	ATT MOUL WICH DINGING INIONIMATION			
Conservancy	Frequency	Protein	Position	Sequence	A4	À*1101	SeqID Num
82	17	절	721	AACFARSR	80		2533
95	19	전	632	AAPFTQCGY	O		2534
06	18		776	ADDPSHGR	89		2535
95	19	절	529	AFPHCLAFSY	10		2536
06	19	×	62	AFSSAGPCALR	Ξ		2537
95	19	정	655	AFTFSPTY	80		2538
95	19	POL	655	AFTESPTYK	6		2539
80	. 16	ENA	180	AGFFLITR	80		2540
95	19	<u>S</u>	18	AGPLEEELPR	10		2541
95	19	<u>გ</u>	521	AICSWRR	80		2542
95	19	SE SE	41	ALESPEHCSPH	11		2543
06	18	P.	772	ALNPADDPSR	10		2544
85	17	×	70	ALRFTSAR	8		2545
80	16	ENA	108	AMOWNSTTFH	10		2546
80	80	POL	166	ASFOGSPY	80		2547
80	16	<u>8</u>	822	ASPLHVAWR	თ		2548
75	15	ENA	84	ASTNROSGR	o		2549
80	16	<u>8</u>	755	CAANWILP	80		2550
85	17	×	69	CALRETSAR	6		2551
80	16	×	9	CCGLDPAR	80		2552
75	15	절	607	CFRIALPVNR	6		2553
95	19	절	638	CGYPALMPLY	10		2554
95	19	EN	253	CLIFLLVLLDY	==		2555
06	18	×	17	CLRPVGAESR	10		2556
100	20	SP.	48	CSPHHTALR	6		2557
95	19	Ą.	523	CSVVRRAFPH	10		2558
06	18	졏	540	DDVVLGAK	æ		2559
85	17	2	59	DLLDTASALY	10		2560
85	17	SEC MEC	29	DLLDTASALYR	11		2561
90	18	ğ	737	DNSVVLSR	80		2562
06	18	<u>S</u>	131	DNSVVLSRK	6		2562
90	18	<u>S</u>	737	DNSVVLSRKY	10		2533
85	17	SE SE	32	DTASALYR	80		2534
95	19	절	418	DVSAAFYH	80		2535
90	18	Z Z	541	DVVLGAKSVQH	=		2536
95	19	ğ	17	EAGPLEEELPR	11		2537
06	18	2	40	EALESPEH	. 60		2538
06	18	전	718	ELLAACFAR	6		2539
85	17	<u>8</u>	718	ELLAACFARSR	==		2540
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Table XVII A11 Motif With Binding Information

Conservancy	Frequency	Protein	Position	Sequence	ΥΥ	A.1101	SeqiD Num
į	4	9	:		ć		1430
95	<u>-</u>	2	43	ESPEHCSPH	æ.		1967
95	19	SEC PEC	43	ESPEHCSPHH	0		2542
95	19	NC	174	ETTVVRRR	80		2543
80	16	NC	174	ETTWRARGA	10		2544
95	19	<u>S</u>	631	FAAPFTQCGY	10		2545
80	16	<u>8</u>	821	FASPLHVAWR	10		2546
75	15	NC	139	FGRETVLEY	თ		2547
75	. 15	<u>8</u>	244	FGVEPSGSGH	10		2548
98	19	NC	122	FGVWIRTPPAY	=		2549
95	19	<u>8</u>	562	FLLSLGIH	80		2550
95	19	ENA	256	FLLVLLDY	° 60		2551
100	20	졏	363	FLVDKVPH	80		2552
06	18	×	63	FSSAGPCALR	10		2553
95	19	ğ	656	FTFSPTYK	80		2554
95	19	<u>R</u>	518	FTSAICSWR	10		2555
95	19	<u>S</u>	518	FTSAICSVVRR	Ξ		2556
95	19	×	. 132	FALGGORH	æ		2557
06	18	×	132	FVLGGCRHK	o		2558
80	16	PO	754	GCAANWILR	6		2559
95	19.	Š.	630	GFAAPFTQCGY	Ξ		2560
100	50	절	360	GGVFLVDK	æ		2561
100	50	Š	360	GGVFLVDKNPH	Ξ		2562
75	15	PQ.	267	GIHLNPNK	æ		2563
75	15	P _O	567	GIHLNPNKTK	10		2564
75	15	정	567	GIHLNPNKTKR	Ξ		2565
85	17	NC	29	GMDIDPYK	æ		2566
98	19	절	44	GNLNVSIPWTH	Ξ		2567
06	18	절	735	GTDNSVVLSR	10		2568
90	18	전	735	GTDNSVVLSRK	Ξ		2569
80	16	정	245	GVEPSGSGH	6		2570
100	50	정	361	GVFLVDKNPH	10	٠	2571
95	19	N.	123	GVWIRTPPAY	10		2572
95	19	MC	123	GVWIRTPPAYR	Ξ		2573
100	20	NC	47	HCSPHHTALR	10		2574
80	16	ğ	820	HFASPLHVAWR	Ξ		2575
92	19	×	49	HGAHLSLR	80		2576
06	18	NC	104	HISOLTFGR	6		2577
75	15	ᅙ	569	HLNPNKTK	æ		2578
7.5	15	집	569	HLNPNKTKR	6		2579

Table XVII A11 Motif With Binding Information

			=	All Motif With Binding information			
Conservancy	Frequency	Protein	Position	Sequence	AA	A*1101	SeqID Num
	ć	Š	•	A notation as i	÷		0830
3	02	₹	94-	HILWKAGILY	2 :		2007
100	50	ರ್	149	HTLWKAGILYK	Ξ		2581
92	19	절	522	ICSVVRRAFPH	Ξ		2582
90	18	절	617	IDWKVCQR	89		2583
100	20	EN	381	IFFCLWYY	80		2584
. 95	19	EN	255	(FLLVLLDY	6		.2585
80	16	전	734	IGTDNSVVLSR	Ξ		2586
80	. 16	정	260	ILRGTSFVY	6		2587
06	18	NC	105	ISOLTEGR	80		2588
100	20	<u>p</u>	153	KAGILYKR	89		2589
75	15	δ	108	KLIMPARFY	6		2590
80	16	PQ	610	KLPVNRPIDWK	=		2591
75	15	×	130	KVFVLGGCR	o		2592
75	15	×	130	KVFVLGGCRH	10		2593
95	19	20.	55	KVGNFTGLY	6		2594
85	17	ğ	720	LAACFARSR	6		2595
06	18	×	16	LCLRPVGAESR	Ξ		2596
100	20	젛	125	LDKGIKPY	80		2597
100	20	젛	125	LDKGIKPYY	6		2598
80	91	×	တ	LDPARDVLCLR	. =		2599
85	17	NC NC	31	LDTASALY	89		2600
85	17	SEC SEC	31	LDTASALYR	o		2601
95	19	정	417	LDVSAAFY	89		2602
95	19	졏	417	LDVSAAFYH	6		2603
95	19	절	544	LGAKSVQH	80		2604
80	16	PQ.	753	LGCAANWILR	10		2605
7.5	15	전	999	LGIHLNPNK	6		2606
75	15	정	266	LGIHLNPNKTK	=		2607
95	19	EN	254	LIFLLVLLDY	01		2608
100	20	정	109	LIMPARFY	80		5609
06	18	전	719	LLAACFAR	80		2610
85	17	PQ.	719	LLAACFARSR	10		2611
85	17	SE SE	30	LLDTASALY	6		2612
85	17	NC	30	LLDTASALYR ·	10		2613
80	16	PQ.	752	LLGCAANWILR	Ξ		2614
100	20	ENS	378	LLPIFFCLWVY	=		2615
06	18	<u>S</u>	773	LNPADDPSR	6		2616
06	18	PQ.	773	LNPADDPSRGR	=		2617
75	15	전	270	LNPNKTKR	80		2618

Table XVII A11 Motif With Binding Information

15 POL 1 1 1 1 1 1 1 1 1		ı						
15 POL STO LIMMSTRANCY 11 11 11 11 11 11 11	Conservancy	Frequency	Protein	Position	Sequence	AA	A-1101	SeqID Num
19 POL 46 LUNSIPWTH 11		ų,	į			;		0.00
19 POL 46 LUNSEWTHK 11	2	2	POL	220	LNPNKTKRWGY	Ξ		6192
19 POL 46 LINSIPHTH 10	വ	19	ᅙ	46	LNVSIPWTH	Ξ		2620
19 POL 415 LSLDVSAAPY 11 11 15 10 11 15 10 15 15	2	19	절	46	LNVSIPWTHK	10		2621
19 POL 415 LSLOWSANPH 11 19 NLC 164 LSLOWSANPH 11 19 NLC 163 LSLOWERK 11 10 NLC 137 LTFGRENLEY 11 11 POL 137 LTFGRENLEY 11 12 POL 239 LUNBSORRH 9 13 K 103 MATHOMACK 9 14 POL 237 LUNBSORRH 9 15 X 103 MATHOMACK 9 16 K 216 NAUNSIPWTH 9 17 ERW 215 NAUNSIPWTH 9 18 POL 738 NAUNSIPWTH 9 19 POL 45 NAUNSIPWTH 9 10 FOL 738 NAUNSIPWTH 9 11 FOL 738 NAUNSIPWTH 9 12 ERW 215 NAUNSIPWTH 9 13 POL 775 POLONSRIGH 9 14 POL 775 POLONSRIGH 9 15 ERW 233 POSTRAWAL 9 16 POL 477 NAUNSIPWTH 9 17 X 68 POSTRAWAL 9 18 POL 775 POLONSRIGH 9 19 ERW 233 POSTRAWAL 9 10 POL 124 PULGREPY 10 10 POL 124 PULGREPY 10 11 POL 124 PULGREPY 10 12 POL 20 PULGREPH 9 20 POL 124 PULGREPY 10 21 POL 20 PULGREPH 9 22 POL 124 PULGREPH 9 23 POL 124 PULGREPH 9 24 POL 124 PULGREPH 9 25 POL 124 PULGREPH 9 26 POL 124 PULGREPH 9 27 PULGREPH 9 28 POL 124 PULGREPH 9 29 POL 124 PULGREPH 9 20 POL 124 PULGREPH 9 21 POL 124 PULGREPH 9 22 POL 124 PULGREPH 9 23 PULGREPH 9 24 PULGREPH 9 25 POL 124 PULGREPH 9 26 POL 124 PULGREPH 9 27 PULGREPH 9 28 PULGREPH 9 29 PULGREPH 9 20 POL 124 PULGREPH 9 20 PULGREPH 9 21 PULGREPH 9 22 PULGREPH 9 23 PULGREPH 9 24 PULGREPH 9 25 PULGREPH 9 25 PULGREPH 9 26 PULGREPH 9 27 PULGREPH 9 28 PULGREPH 9 29 PULGREPH 9 20 PULGR	5	19	젛	415	LSLDVSAAFY	10		2622
15 POL 564 LS.GHUJPPIK 11 15 NUC 169 LS.GPHUJPPIK 11 15 NUC 137 LIVERFINAT 11 17 POL 137 LIVERFINAT 11 18 POL 137 LIVERFINAT 10 18 POL 539 MADDIVICARY 9 19 POL 561 MATTOLEAMY 9 19 POL 561 MATTOLEAMY 9 19 POL 561 MATTOLEAMY 9 10 POL 561 MATTOLEAMY 9 10 POL 45 MATTOLEAMY 9 11 POL 561 MATTOLEAMY 9 12 POL 47 MASPAWTH 9 13 POL 47 MASPAWTH 9 14 POL 47 MASPAWTH 9 15 ENV 233 POSTRAGOSAR 10 16 POL 546 PULMCIRY 9 17 X 68 POL 616 PULMCIRY 9 18 POL 233 POSTRAGOSAR 10 19 POL 246 PULMCIRY 9 10 POL 246 PULMCIRY 9 11 POL 616 PULMCIRY 8 12 POL 246 PULMCIRY 9 13 POL 247 PULMCIRY 9 14 PULMCIRY 9 15 POL 248 PULMCIRY 9 16 POL 249 PULMCIRY 9 17 PULMCIRY 9 18 POL 240 PULMCIRY 9 19 POL 247 PULMCIRY 9 19 POL 247 PULMCIRY 9 19 POL 247 PULMCIRY 9 10 PULMCIRY 9 11 POL 240 PULMCIRY 9 12 PULMCIRY 9 13 POL 240 PULMCIRY 9 24 PULMCIRY 9 25 PULMCIRY 9 25 PULMCIRY 9 26 PULMCIRY 9 27 PULMCIRY 9 28 PULMCIRY 9 29 PULMCIRY 9 20 PUL	2	19	<u>5</u>	415	LSLDVSAAFYH	=======================================		2623
15 NLC 169 LSTUPETTVNR 11 11 11 12 12 12 12 1	5	15	정	564	LSLGIHLNPNK	-1		2624
15 POL 3 LISOFFER 1 15 NLC 193 LISOFFER 1 18 NLC 119 LISOFFER 1 18 POL 539 MADDVLGAR 9 19 POL 539 MASTDLEAY 10 15 X 103 MASTDLEAY 9 15 X 103 MASTDLEAY 11 16 NLC 561 NLLSGIH 9 19 POL 561 NLLSGIH 9 19 POL 45 NLLSGIH 9 19 POL 45 NLLSGIH 9 10 POL 45 NLLSGIH 9 10 POL 738 NLNSIPWTH 9 11 POL 738 NLNSIPWTH 9 12 POL 47 NVSIPWTH 9 13 POL 47 NVSIPWTH 9 14 POL 47 NVSIPWTH 9 15 ENV 233 POSTBAR 9 16 X 11 PARDVLCH 9 16 X 233 POSTBWADA 9 17 X 68 POLMFTSAR 10 18 POL 446 PULGFFK 9 19 POL 446 PULGFFK 9 10 POL 446 PULGFFK 9 11 POL 124 PULGFFK 9 12 POL 124 PULGFFK 9 13 POL 124 PULGFFK 9 14 POL 124 PULGFFK 9 15 POL 124 PULGFFK 9 16 POL 124 PULGFFK 9 17 POL 124 PULGFFK 9 18 POL 124 PULGFFK 9 19 POL 124 PULGFFK 9 10 POL 124 PULGFFK 9 11 POL 124 PULGFFK 9 12 POL 124 PULGFFK 9 13 POL 124 PULGFFK 9 14 POL 124 PULGFFK 9 15 POL 124 PULGFFK 9 16 POL 124 PULGFFK 9 17 PULGFFK 9 18 POL 124 PULGFFK 9 19 POL 124 PULGFFK 9 10 POL 124 PULGFFK 9 11 POL 124 PULGFFK 9 12 PULGFFK 9 13 PULGFFK 9 14 PULGFFK 9 15 PULGFFK 9 16 PULGFFK 9 17 PULGFFK 9 18 PULGFFK 9 19 PULGFFK 9 10 PULGFFK 9 11 PULGFFK 9 12 PULGFFK 9 13 PULGFFK 9 14 PULGFFK 9 15 PULGFFK 9 16 PULGFFK 9 17 PULGFFK 9 18 PULGFFK 9 18 PULGFKK 9 19 PULGFKK 9 10 PULGFKK 9 11 PULGFKK 9 12 PULGFKK 9 13 PULGFKK 9 14 PULGFKK 9 15 PULGFKKK 9 16 PULGFKKK 9 17 PULGFKKK 9	5	19	NC C	169	LSTLPETTVVR	11		2625
15 NLC 137 LTGBEPULEY 11 17 POL 199 LUNBERNER 19 18 NLC 199 LUNBERNER 9 18 POL 377 LUNGERONER 9 17 ENV 360 NAMWYNGRONER 9 15 X 103 NATIDLEAN 10 16 X 103 NATIDLEAN 11 18 POL 561 NFLEDASH 9 19 POL 45 NUNSIPWITH 10 19 POL 45 NUNSIPWITH 10 10 POL 45 NUNSIPWITH 9 10 POL 47 NUSIPWITH 9 11 POL 738 NUSIPWITH 9 12 POL 775 POLDESIGER 9 13 POL 775 POLDESIGER 9 14 NUSIPWITH 9 15 ENV 233 POTTAMOLA 9 16 POL 47 NUSIPWITH 9 17 X 68 POLDESIGER 10 18 POL 47 NUSIPWITH 9 19 POL 48 POLDESIGER 10 10 POL 49 PULCHIPS 9 11 POL 49 PULCHIPS 9 12 PULCHIPS 9 13 POL 41 PULCHIPS 9 14 PULCHIPS 9 15 POL 49 PULCHIPS 9 16 POL 49 PULCHIPS 9 17 PULCHIPS 9 18 POL 49 PULCHIPS 9 19 POL 47 PULCHIPS 9 10 POL 47 PULCHIPS 9 11 POL 49 PULCHIPS 9 12 PULCHIPS 9 13 POL 47 PULCHIPS 9 14 POL 47 PULCHIPS 9 15 POL 47 PULCHIPS 9 16 POL 47 PULCHIPS 9 17 PULCHIPS 9 18 POL 47 PULCHIPS 9 19 POL 47 PULCHIPS 9 10 POL 47 PULCHIPS 9 11 PULCHIPS 9 12 PULCHIPS 9 13 PULCHIPS 9 14 PULCHIPS 9 15 PULCHIPS 9 16 PULCHIPS 9 17 PULCHIPS 9 18 PULCHIPS 9 19 PULCHIPS 9 10 PULCHIPS 9 11 PULCHIPS 9 12 PULCHIPS 9 13 PULCHIPS 9 14 PULCHIPS 9 15 PULCHIPS 9 16 PULCHIPS 9 17 PULCHIPS 9 18 PULCHIPS 9 18 PULCHIPS 9 18 PULCHIPS 9 19 PULCHIPS 9 10 PULCHIPS 9 11 PULCHIPS 9 12 PULCHIPS 9 13 PULCHIPS 9 14 PULCHIPS 9 15 PULCHIPS 9 15 PULCHIPS 9 16 PULCHIPS 9 17 PULCHIPS 9 18 PULCHIPS 9	75	. 15	절	ო	LSYOHFRK	80		2626
17 POL 99 LIVNEKRR 8 20 POL 377 LIVNEKRR 9 18 POL 539 MADVINGAK 9 17 ENV 360 MANTOLEAN 10 15 X 103 MASTDLEANK 11 16 POL 561 NILNESIPATK 9 19 POL 45 NILNESIPATK 11 10 47 NISOPATK 9 20 POL 47 NISOPATK 9 21 ENV 23 PARDVICLAR 9 22 ENV 23 POLMETSAR 9 23 ENV 23 POLMETSAR 9 24	75	15	NC	137	LTFGRETVLEY	Ξ		2627
18 NLC 119 LVSFGWNH 9 20 POL 537 LVMPSGASR 10 18 POL 539 MAMYMGPSLY 10 15 X 103 MATTDLEAYR 9 15 X 103 MATTDLEAYR 11 19 POL 561 NFLSLGIH 11 19 POL 45 NLANSIPWTH 11 19 POL 45 NLANSIPWTH 11 19 POL 45 NLANSIPWTH 9 10 POL 45 NLANSIPWTH 9 10 POL 47 NVSIPWTH 9 10 POL 47 NVSIPWTH 9 10 A NVSIPWTH 9 10 A NVSIPWTH 9 11 POL 47 NVSIPWTH 9 12 ENV 83 POSTMANSAR 9 13 ENV 2	85	17	ᅙ	66	LTVNEKRR	æ		2628
20 POL 377 LWOPSGESH 10 17 ENV 589 MANTWARSLY 10 15 X 103 MASTTDLEAY 10 19 POL 561 NIELBASH 9 19 POL 45 NILEDRAYK 11 19 POL 45 NILEDRAYK 10 19 POL 45 NILEDRAYK 11 10 NILEDRAYK 11 10 10 NILEDRAYK 11 10 10 NILEDRAYK 9 9 10 NILEDRAYK 9 9 10 NILEDRAYK 9 9 10 NILEDRAYK 9 10 10 NILEDRAYK 10 10 10	90	18	NC	119	LVSFGVWIR	o		2629
18 POL 539 MANDVULGAK 9 17 KEW 360 MANDVULGAK 10 15 X 103 MASTTDLEAYF 9 19 NC 561 MASTTDLEAYF 9 19 NC 561 MASTTDLEAYF 11 19 POL 45 MUNSIPWTH 10 19 POL 45 MUNSIPWTH 11 18 POL 738 NUNSIPWTH 9 18 POL 738 NUNSIPWTH 9 20 POL 47 NUSIPWTH 9 20 POL 47 NUSIPWTH 9 20 POL 47 NUSIPWTH 9 20 ENV 23 POLDSPSGAR 10 21 X 11 PADDVLCAR 9 22 ENV 233 POTRAMACAR 9 23 POL 436 PULGRAM 9	ō	20	ğ	377	LWDFSQFSR	10		2630
17 ENV 360 MAMWWAGPSLY 10 15 X 103 MSTDLEAY 11 19 POL 561 NILEDSIGH 9 19 POL 45 NILEDSIGH 9 19 POL 45 NILEDSIGH 11 19 POL 45 NILEDSIGH 9 18 POL 45 NILEDSIGH 11 19 POL 45 NILEDSIGH 11 10 AC NILEDPASH 11 11 11 NILEDPASH 11 11 11 12 NILEDPASH 11 11 11 11 13 NILEDPASH 11<	0	18	정	539	MDDVVLGAK	o		2631
15 X 103 MSTTDLEAY 9 15 X 103 MSTTDLEAYEK 11 19 POL 561 NFLEDPASH 9 18 NLC 75 NLMSIPWTH 10 19 POL 45 NLMSIPWTH 10 18 POL 215 NSVASHWTH 9 18 POL 738 NSVALSRY 9 20 POL 47 NVSIPWTH 9 20 POL 47 NVSIPWTH 9 20 POL 47 NVSIPWTH 9 16 A 11 PADDPSRGR 9 16 A NSTALBYTSAR 10 16 A NSTALBYTSAR 10 17 X 68 PCALBTSAR 10 18 POL 616 POLMARANA 9 19 POL 616 PULKGRAYA 9 20 POL 124		17	ENA	360	MMMYWGPSLY	10		2632
15 X 103 MSTDLEAVFK 11 19 POL 561 NRLSLGIH 9 18 NLC 75 NILEDRASH 8 19 POL 45 NILEDRASH 10 19 POL 45 NILEDRASH 11 16 ENV 215 NOSOPTSNH 11 18 POL 73 NISVILSBRK 9 20 POL 47 NUSIPWTH 9 20 POL 47 NUSIPWTH 9 16 X 11 PASTNASSRA 9 16 X 11 PASTNASSRA 9 16 X 11 PASTNASSRA 10 17 X 68 PCALAFTSAR 10 20 ENV 23 PCATRATASAR 10 21 FN 23 PCATRATASAR 9 22 ENV 23 PCATRATASAR 9 <td< td=""><td></td><td>15</td><td>×</td><td>103</td><td>MSTTDLEAY</td><td>Ø</td><td></td><td>2633</td></td<>		15	×	103	MSTTDLEAY	Ø		2633
19 POL 561 NFLESIGH 9 18 NAC 75 NLEDPASR 8 19 POL 45 NULNOSIPWTH 10 19 POL 45 NULNOSIPWTH 11 16 ENV 215 NSOVESTAM 9 18 POL 738 NSVALSRK 9 20 POL 47 NVSIPWTH 9 20 POL 47 NVSIPWTH 9 18 POL 47 NVSIPWTH 9 10 X 11 PADDPSRGR 9 15 ENV 83 PASTRAGSGR 10 16 X 11 PASTRAGSGR 9 20 ENV 233 PCATRTSAR 9 21 POL 436 PULCAPRA 9 20 ENV 233 PORTAMACAR 9 20 POL 124 PULCAPRA 9 20		15	×	103	MSTTDLEAYFK	=		2634
18 NLC 75 NLEDPASH 8 19 POL 45 NUNVSIPWTH 10 19 POL 45 NUNVSIPWTH 11 18 POL 738 NSVVLSRY 8 18 POL 47 NVSIPWTH 9 20 POL 47 NVSIPWTH 9 18 POL 775 PADDOSRGR 9 16 X 11 PARDVLCLR 9 15 EKW 233 POTRFTSAR 10 20 EKW 233 POTRFTSAR 9 19 EW 233 POTRFTSAR 9 20 EW 233 POTRFTSAR 9 20 EW 233 POTRFTSAR 9 20 EW 235 POTRFTWAY 9 20 POL 124 PULKGHPY 9 20 POL 124 PULKGHPY 9 20 </td <td></td> <td>19</td> <td>젛</td> <td>561</td> <td>NFLLSLGIH</td> <td>6</td> <td></td> <td>2635</td>		19	젛	561	NFLLSLGIH	6		2635
19 POL 45 NLNVSIPWTH 10 19 POL 45 NLNVSIPWTHK 11 18 POL 738 NSVLSRY 8 20 POL 47 NVSIPWTH 9 20 POL 47 NVSIPWTHK 9 20 POL 47 NVSIPWTHK 9 18 POL 775 PADDPSRGR 9 16 X 11 PASTNACOSR 9 15 ENV 83 POSTNAMOLAR 10 20 ENV 233 POSTNAMOLAR 10 18 POL 616 PONMONOCAR 9 20 ENV 233 POSTNAMOLAR 9 20 ENV 380 PIEFCLANY 9 20 POL 124 PLDKGIKPY 9 20 POL 124 PLDKGIKPY 9 20 POL 124 PLDKGIKPY 9	_	18	NC	75	NLEDPASH .	80		2636
19 POL 45 NLNVSIPWTHK 11 16 ENV 215 NSQSPTSNH 9 18 POL 738 NSVLSRKY 9 20 POL 47 NVSIPWTHK 9 20 POL 47 NVSIPWTHK 9 20 POL 47 NVSIPWTHK 9 18 POL 775 PADPPSKGR 9 15 ENV 83 PASTRATSAR 10 20 ENV 233 PGYRWACJAR 10 19 ENV 233 PGYRWACJAR 10 20 ENV 235 PGYRWACJAR 9 16 POL 436 PHIGFRK 8 20 POL 124 PLDKGIRPY 9		19	절	45	NLNVSIPWTH	10.		2637
15 ENV 215 NSGSPTSNH 9 18 POL 738 NSVLSRK 8 20 POL 47 NVSIPWTH 9 20 POL 47 NVSIPWTH 9 18 POL 775 PARDVLCIR 9 16 X 11 PARDVLCIR 9 17 X 68 PCALPTSAR 10 20 ENV 233 PGYRWACJR 10 19 ENV 233 PGYRWACJR 9 20 ENV 330 PGYRWACJR 9 20 ENV 380 PIFFCLWYY 9 20 POL 124 PLDKGIRPY 10 20 POL 124 PLEEELPR 8 20 POL 124 PLEEELPR 8 20 POL 124 PLEEELPR 9 20 POL 124 PLEEELPR 9 20 </td <td></td> <td>19</td> <td>전</td> <td>45</td> <td>NLNVSIPWTHK</td> <td>=</td> <td></td> <td>2638</td>		19	전	45	NLNVSIPWTHK	=		2638
18 POL 738 NSVVLSRKY 8 20 POL 47 NVSIPWTH 8 20 POL 47 NVSIPWTHK 9 18 POL 47 NVSIPWTHK 9 16 X 11 PADDPSMGR 9 15 ENV 83 PASTNFGGGR 10 20 ENV 233 PGTABFTSAR 9 20 ENV 233 PGTRAMACJAR 10 19 ENV 233 PGTRAMACJAR 9 20 ENV 330 PILGFRK 9 20 ENV 336 PILGFRK 8 20 POL 124 PLINGIRPY 9		15	ENS	215	NSOSPTSNH	თ		2639
18 POL 738 NSVNLSRKY 9 20 POL 47 NVSIPWTH 8 20 POL 47 NVSIPWTHK 9 18 POL 775 PADDPSRGR 9 16 X 11 PADDPSRGR 9 15 ENV 233 PGATHARGAGR 10 20 ENV 233 PGYRAMACHR 9 19 ENV 233 PGYRAMACHR 9 20 ENV 380 PIFFCLWY 9 20 POL 436 PIFCLWY 9 20 POL 124 PLDKGIRYY 9 20 POL 124 PLEFELPR 9 19 POL 124 PLEFELPR 9 20 POL 10 PLEFELPR 9 20 POL 10 PLEFELPR 9 20 POL 10 PLGFPPDH 9 20<	_	18	ᅙ	738	NSVVLSRK	80		2640
20 POL 47 NVSIPWTH 8 20 POL 47 NVSIPWTHK 9 18 POL 775 PADDPSRGR 9 16 X 11 PARDVLCLR 9 15 ENV 83 PASTNRGSGR 10 17 X 68 PASTNRGSGR 10 20 ENV 233 PGYRWACJR 9 19 ENV 233 PGYRWACJR 9 10 ENV 233 PGYRWACJR 9 20 ENV 233 PGYRWACJR 9 16 POL 616 PIDKGKY 9 20 POL 124 PLDKGKPY 9 20 POL 124 PLDKGKPY 9 20 POL 124 PLDKGKPY 9 20 POL 10 PLGFFEUR 9 20 POL 10 PLGFFEUR 9 20 <td>_</td> <td>18</td> <td>豆</td> <td>738</td> <td>NSVVLSRKY</td> <td>6</td> <td></td> <td>2641</td>	_	18	豆	738	NSVVLSRKY	6		2641
20 POL 47 NVSIPWTHK 9 18 POL 775 PADDPSRGR 9 16 X 11 PARDVLCLR 9 15 ENV 83 PASTNROSGR 10 17 X 68 PCALRFTSAR 10 20 ENV 233 PGYRMMCJR 9 18 FOL 616 PITFCLWYY 9 20 ENV 380 PITFCLWYY 9 20 POL 124 PLDKGIRPYY 10 20 POL 124 PLDKGIRPYY 10 20 POL 10 PLGFEDPR 8 20 POL 10 PLGFEDPR 9 20 POL 10 PLGFEDPR 9	0	20	<u>8</u>	47	NVSIPWTH	89		2642
18 POL 775 PADDPSRGR 9 16 X 11 PARDVLCLR 9 15 ENV 83 PASTNAROSGR 10 20 ENV 233 PGYRWMCJR 10 19 ENV 233 PGYRWMCJR 9 20 ENV 380 PIFFCLWY 9 16 POL 496 PILGFRK 9 20 POL 124 PLDKGIKPY 9 20 POL 124 PLDKGIKPY 10 19 POL 20 PLEELPR 8 20 POL 10 PLDKGIKPY 10 20 POL 20 PLDKGIKPY 10 20 POL 10 PLDKGIKPY 10 20 POL 10 PLDKGIKPY 9 20 POL 10 PLDKGIKPY 9 20 POL 10 PLDKGIKPY 9 <td< td=""><td>0</td><td>20</td><td>전</td><td>47</td><td>NVSIPWTHK</td><td>6</td><td></td><td>2643</td></td<>	0	20	전	47	NVSIPWTHK	6		2643
16 X 11 PARDULCLR 9 15 ENV 83 PASTNROSGR 10 20 ENV 233 PGYRAMACJR 9 19 ENV 233 PGYRAMACJRR 9 18 POL 616 PILGFRA 9 20 ENV 380 PILGFRA 9 20 POL 124 PLDKGIKPY 9 20 POL 124 PLDKGIKPY 10 19 POL 10 PLEFELPR 8 20 POL 10 PLEFELPR 8 20 POL 10 PLGFFPDH 9	_	18	ğ	775	PADDPSRGR	6		2644
15 ENV 83 PASTNRAGGR 10 17 X 68 PCALAFTSAR 10 20 ENV 233 PGYRWMCJAR 9 19 ENV 233 PGYRWMCJAR 10 20 ENV 233 PGYRWMCJAR 9 16 POL 436 PIFFCLWYY 9 20 POL 124 PLDKGIKPY 9 20 POL 124 PLDKGIKPY 10 19 POL 20 PLEELPR 8 19 POL 10 PLGFFPDH 9 20 POL 10 PLAPAAMPH 9	_	16	×	Ξ	PARDVLCLR	6		2645
17 X 68 PCALAFTSAR 10 20 ENV 233 PGYRWMCJAR 9 19 ENV 233 PGYRWMCJAR 10 18 POL 616 PIDWKVCQR 9 20 ENV 380 PIFFCLWYY 9 20 POL 124 PLDKGIKPY 9 20 POL 124 PLDKGIKPY 10 19 POL 20 PLEEELPR 8 19 POL 10 PLGFFPDH 9 20 POL 10 PLAPAAMPH 9	10	15	ENA	83	PASTNROSGR	10		2646
20 ENV 233 RGYRWACJR 9 19 ENV 233 PGYRWACJRR 10 18 POL 616 PIDWKVCQR 9 20 ENV 380 PIFFCLWYY 9 20 POL 124 PLDKGIRPY 9 20 POL 124 PLDKGIRPY 10 19 POL 20 PLEFELPR 8 19 POL 10 PLGFFPDH 9 20 POL 10 PLAPAMPH 9	10	17	×	89	PCALRFTSAR .	10		2647
19 ENV 233 PGYRAMAGIAR 10 18 POL 616 PIDWKVCQR 9 20 ENV 380 PIFFGLWY 9 16 POL 496 PILGFRK 8 20 POL 124 PLDKGIKPY 10 19 POL 20 PLEEELPR 8 19 POL 10 PLGFFPDH 9 20 POL 427 PLHPAAMPH 9	0	20	ENA	233	PGYRWMOLR	o		2648
18 POL 616 PIDWKVCQR 9 20 ENV 380 PIFFCLWVY 9 16 POL 496 PILGFPK 9 20 POL 124 PLDKGIKPY 9 20 POL 124 PLEEELPR 10 19 POL 10 PLGFFPDH 8 20 POL 427 PLPAAMPH 9	ıo	19	ENA	233	PGYRWMCLPR	10		2649
20 ENV 380 PIFCLWVY 9 16 POL 496 PILGFRK 8 20 POL 124 PLDKGIKPY 9 20 POL 124 PLEELPR 10 19 POL 10 PLEELPR 8 20 POL 10 PLGFPDH 9 20 POL 427 PLHPAAMPH 9	0	18	절	616	PIDWKVCQR	6		2650
16 POL 496 PILGFRK 8 20 POL 124 PLDKGIKPYY 9 20 POL 124 PLDKGIKPYY 10 19 POL 20 PLEELPR 8 19 POL 10 PLGFFDH 8 20 POL 427 PLHPAAMPH 9	0	20	ENA	380	PIFFCLWVY	6		2651
20 POL 124 PLDKGIKPY 9 20 POL 124 PLEELPR 10 19 POL 10 PLGFFDH 8 20 POL 427 PLHPAAMPH 9	_	16	전	496	PILGFRK	80		2652
20 POL 124 PLDKGIKPYY 10 19 POL 20 PLEEELPR 8 19 POL 10 PLGFFDH 8 20 POL 427 PLHPAAMPH 9	0	20	전	124	PLDKGIKPY	o		2653
19 POL 20 PLEEELPR 8 19 POL 10 PLGFFDH 8 20 POI 427 PLHPAAMPH 9	0	20	전	124	PLDKGIKPYY	10		2654
19 POL 10 PLGFFPDH 8 20 POI 427 PLHPAAMPH 9	S.	19	전	20	PLEEELPR	80		2655
20 POI 427 PI HPAAMPH 9	S	19	豆	10	PLGFFPDH	80		2656
		50	2	42.7	ргираамри	o		2657

Table XVII A11 Motif With Binding Information

SeqID Num	2658	2659	2660	2661	2662	2663	2664	2665	2666	2667	2668	5669	2670	2671	2672	2673	2674	2675	2676	2677	2678	2679	2680	2681	2682	2683	2684	2685	2686	2687	2688	2689	2690	2691	2692	2693	2694	2692	2696
A-1101																																							
АА	8	o	80	o	o	o	თ .·	o	o	01	6	0	=	Ξ	Ξ	80	=	Ξ	80	o	Ξ	Ξ	Ξ	=	&	တ	80	o	σ	11	80	80	o	=	თ	o	10	10	o
Sequence	PLSYOHFR	PLSYOHFRK	PLTVNEKR	PLTVNEKRR	PNKTKRWGY	PTTGRTSLY	PVGAESRGR	PVNRPIDWK	QAFTFSPTY	QAFTFSPTYK	OAGFFILTR	QAMQWNSTTFH	QCGYPALIMPLY	QFTSAICSWR	CSPRARRSOSR	CSSGILSR	PAFPHCLAFSY	RDLLDTASALY	RGPSPPRR	RLKLIMPAR	RLKLIMPARFY	PLKVFVLGGCR	RLWDFSQFSR	RSPRARTPSPR	RSOSPARA	RSOSPRPRR	RIPSPARA	RIPSPARR	RVHFASPLH	RVTGGVFLVDK	SAGPCALR	SAICSVVR	SAICSWAR	SALNPADDPSR	SASFOGSPY	SLDVSAAFY	SLDVSAAFYH	SLGIHLNPNK	SSAGPCALR
Position	. 0		98	86	572	797	20	612	654	654	179	107	637	517	169	189	528	28	152	106	106	128	376	183	167	167	188	188	818	357	6 9	520	520	77.1	165	416	416	565	64
Protein	젍	절	<u>8</u> .	PoL	∑	<u>S</u>	×	전	전	<u>5</u>	ENV	ËN	절	절	NC	ğ	P _Q	NC	NC	ğ	절	×	정	SP	SE	SPC	SEC	NC S	절	절	×	<u>8</u>	절	집	집	젛	전	젗	×
Frequency	20	15	17	17	15	17	18	. 17	19	19	16	16	19	19	15	16	19	17	20	15	. 15	15	19	19	15	15	19	19	16	20	18	19	19	18	20	19	19	15	81
Conservancy	100	75	85	85	75	85	06	85	98	95	80	80	95	95	75	80	95	85	100	. 275	75	75	98	98	75	75	98	95	80	100	06	98	95	06	100	95	95	75	06

Table XVII A11 Motif With Binding Information

			-				
Conservancy	Frequency	Protein	Position	Sequence	AA	A*1101 S	SeqID Num
							ľ
95	19	NC	170	STLPETTVVR	10		2697
95	19	NC	170	STLPETTVVRR	Ξ		2698
80	16	ENA	82	STINFOSGR	80		5698
75	15	×	104	STTDLEAY	æ		2700
75	15	×	104	STTDLEAYFK	10		2701
06	18	<u>5</u>	739	SWLSRKY	80		2702
95	19	전	524	SWRRAFPH	6 1		2703
85	. 17	전	716	TAELLAACFAR	=		2704
80	16	×	106	TDLEAYFK	8		2705
06	18	전	736	TDNSVVLSR	o		2706
06	18	전	736	TDNSVVLSRK	10		2707
06	18	정	736	TDNSVVLSRKY	Ξ		2708
75	15	NC NC	138	TFGRETVLEY	10		2709
100	20	ğ	359	TGGVFLVDK	6		2710
95	19	SEC MEC	171	TLPETTVVR	o		2711
95	19	NUC	171	TLPETTVVRR	10		2712
95	19	SE SE	171	TLPETTVVRRR	=		2713
100	50	전	150	TLWKAGILY	6		2714
100	20	절	150	TLWKAGILYK	10		2715
100	50	δ	150	TLWKAGILYKR	=		2716
95	19	절	260	TNFLLSLGIH	10		2717
95	19	ğ	519	TSAICSVVR	6		2718
95	19	절	519	TSAICSVVRR	10		2719
75	15	×	105	TTDLEAYFK	o		2720
85	17	절	798	TTGRTSLY	&		2721
75	15	EN	278	TTSTGPCK	80		2722
80	16	N.	175	TTWRAGA	6		2723
80	16	SEC SEC	176	TWARRGR	80		2724
80	16	SEC C	176	TWRRAGRSPR	=		2725
100	20	정	379	VDFSQFSR	æ		2726
100	50	젗	362	VFLVDKNPH	o		2727
80	16	×	131	VFVLGGCR	89		2728
80	16	×	131	VFVLGGCRH	6		2729
75	15	×	131	VPVLGGCRHK	10		2730
95	19	×	21	VGAESRGR	80		2731
95	19	전	56	VGNFTGLY	80		2732
85	17	ğ	96	VGPLTVNEK	o		2733
85	17	정	96	VGPLTVNEKR	10		2734
85	17	ğ	96	VGPLTVNEKRR	=		2735

Table XVII A11 Motif With Binding Information

Conservancy	Frequency	Protein	Position	Sequence	AA	A-1101	SeqID Num
	,						3070
66	<u>.</u>	Į.	543	VLGAKSVQH	י מ		27.30
06	48	×	133	VLGGCRHK	œ		2737
80	16	EN	177	VLQAGFFLLTR	=		2738
85	17	정	613	VNRPIDWK	80		2739
06	18	NC NC	120	VSFGVWIR	œ		2740
100	20	₽	48	VSIPWTHK	æ		2741
100	20	Z Z	358	VTGGVFLVDK	. 10		2742
100	50	PO	378	WDFSQFSR	o		2743
06	18	절	542	VVLGAKSVQH	10		2744
95	19	Š	525	VVRRAFPH	60		2745
80	16	SPC NPC	177	WARAGASPR			2746
80	16	NC N	177	WARAGASPAR	11		2747
06	18	S)N	102	WFHISCLIFGR	=		2748
85	17	NC N	. 82	WGMDIDPY	œ		2749
85	17	NC	28	WGMDIDPYK	6		2750
85	17	전	578	WGYSLNFMGY	10		2751
80	16	Z Z	759	WILRGTSFVY	10		2752
95	19	NUC	125	WIRTPPAY	80		2753
95	19	NUC	125	WIRTPPAYR	o		2754
06	8	PQ.	314	WLOFRNSK	80		2755
95	19	POL	414	WLSLDVSAAFY	11		2756
85	17	N N	56	WLWGMDIDPY	10		2757
85	17	NC	26	WLWGMDIDPYK	11		2758
85	17	EN	359	WMMWYWGPSLY	==		2759
100	20	절	122	YLPLDKGIK	6		2760
100	20	δ	122	YLPLDKGIKPY	==		2761
06	18	N N	118	YLVSFGVWIR	10		2762
06	18	전	538	YMDDVVLGAK	10		2763
80	16	전	493	YSHPILGFR	10		2764
80	16	전	493	YSHPIILGFRK	Ξ		2765
85	17	정	580	YSLNFWGY	80		2766

0.0004 0.0012 0.0310 0.0024 A*2401 0.0007 0.0087 Filed A A HBV A24 Motif With Binding Information SEQ ID 2773 2775 2776 2777 2778 2779 2780 2781 2781 2783 2784 2785 2786 2787 2788 2789 2789 2790 2791 2792 2793 2793 2795 2796 2797 2798 2799 2800 2802 2803 2805 ÿ FFPDHQLDPAF GFFLLTRI HYLHTLWKAGI IFFCLWVYI AFTESPTYKAF DYGGMLPVCPL EYLVSFGVW EYLVSFGVWI GYRWMCLRRF GYRWINCLRRFI **GYSLNFMGYVI HFASPLHVAW** WMMWWGPSI DWKVCQRIVGL GFFLLTRIL GFFLLTRILTI GFFDHOL KYLPLDKGI KYTSFPWL CFRKLPVNRPI GFRKIPMGVGL AFSYMDDVVL GWSPQAQGIL KFAVPNLOSL AFSSAGPCAL **AMQWNSTTF** AYRPPNAPI AYRPPNAPIL FFCLWYII FFLLTRIL GMDIDPYKEF GWLWGMDI GWSPOAGGI DWKVCQRI FFLLTRILTI GFLGPULM. GMLPVCPL GYPALMPL FLFILL HFRKLLL Sequence Position 181 181 12 170 5500 29 265 25 65 65 639 234 234 234 234 820 182 Protein Freq. Table XVIII Conservancy

0900.0 0.0099 0.0002 0.0710 1.1000 0.0710 0.3900 5.6000 0.0005 A-2401 5.3000 1.1000 0.0290 Filed ٩ HBV A24 Motif With Binding Information SEO IO 2842 2843 2845 2846 2813 2844 2814 2815 2816 2818 2820 2822 2841 2847 2817 PWLLGCAANWI PWTHKVGNF PFVQWFVGL PMGVGLSPF PMGVGLSPFL PMGVGLSPFLL SWLSLLVPF SWPKFAVPNL SWMTSLNF OWFVGLSPTVW SWLSLDVSAAF **PWLLGCAANW** SFCGSPYSW SFLPSDFF **PFLLAQFTSAI** RFSWLSLLVPF RWMCLRRFIIF LYSHPIIL LYSHPIILGF **PFTQCGYPAL** MMWWGPSL RFIIFLFILL RFIIFLFILLL RWMCLRRFII RWMCLRRFI LWFHISCLTF MWYWGPSL NFLLSLGIHL NWILIGITSF **PWGYSLNF** RWACLRRF SFVYVPSAL FILLCLIFL RFIIFLFI KYTSFPWLL LFILLCLF LMPLYACI NFLLSLGI RFIIFLFIL RFSWLSLL LFILLICLI LWFHISCL Sequence Position 561 Protein Freq. Table XVIII Conservancy 95 80 80 80 80 80 100 100 100 95 95 95 95 95 95 95 95 95 95 95

Conservancy	Freq.	Protein	Position	Sequence	SEQ ID NO:	٧٧	Filed	A*2401
95	19	WB	197	SWMTSLNFL	2853	б	•	0.3800
06	18	정	537	SYMDDVVL	2854	8		
7.5	15	<u>ದ</u>	4	SYQHFRKL	2855	80		
7.5	15	전	4	SYQHFRKLL	2856	6		0.0051
75	15	젍	4	SYCHFRKLLL	2857	. 10	•	0.0660
75	15	ጃ	4	SYQHFRKLLLL	2858	11		
75	15	S)	138	TFGRETVL	2859	60		
7.5	15	3	138	TFGRETVLEYL	2860	11		
95	19	S.	657	TFSPTYKAF	2861			0900.0
98	19	젍	657	TFSPTYKAFL	2862	10		0.0043
95	19	ರ್ಷ	989	VFADATPTGW	2863	10	•	0.0180
7.5	15	×	131	VFVLGGCRHKL	2864	=		
	18	SQ.	102	WFHISCLTF	2865	တ	•	0.0300
96	19	AB.	345	WFVGLSPTVW	2866	10	•	0.0120
95	19	æ	345	WFVGLSPTVWL	2867	-		
95	19	A A	237	WMCLRRFI	2868	00		
95	19	A Ma Ma Ma Ma Ma Ma Ma Ma Ma Ma Ma Ma Ma	237	WMCLRRFII	2869	თ		
98	19	26	237	WMCLRRFIIF	2870	10		0.0013
95	19	A N	237	WMCLRRFIIFL	2871	Ξ		
85	17	A N	359	WMMWWGPSL	2872	10		
90	0	à	100	MAATICINE	2873	α		

HBV DR-SUPER MOTIF

Table XIXa

Protein	Core SEQ ID NO:	Core Sequence	Core Freq.	Conservancy (%)	Exemplary SEQ ID NO:	Exemplary Sequence	Position In HBV Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ಭ	2874	FAAPFTOCG	19	95	3021	LLGFAAPFTQCGYPA	. 828	19	95
ಕ	2875	FADATPTGW	19	95	3022	COVFADATPTGWGLA	684	16	80
절	2876	FAVPNLOSL	19	95	3023	WPKFAVPNLQSLTNL	393	19	95
NC	2877	FGRETWEY	15	7.5	3024	CLTFGRETVLEYLVS	136	14	7.0
8	2878	FGVEPSGSG	15	75	3025	RRSFGVEPSGSGHID	252	9	30
S	2879	FHISCLIFG	89	06	3026	LLWFHISOLTFGRET	100	17	85
2	2880	FHLCLIISC	16	80	3027	MOLFHLCLIISCSCP	-	0	20
2	2881	FILLICLIF	9 :	80	3028	FLFILLCLIFLLV	245	9 :	80
2 2	2882	FIFILICE	9 .	80	3029	FIIFLFILLCLIFL	243	9 ,	08.
200	5883	FLGPLVLU	ر د م	ۍ د د	3030	ISGFLGPLLVLQAGF	890	٠ د ۲	ς, c
2 6	1000	יייי אורון	0 9	0 0	3031	AGPITUTION OF THE PARTY OF THE	000	<u>e</u> ç) (0)
	2882	FLLVLLDYQ	5 U	4 4 7	3032	CLIFILVILLDYGGML	253	5 -	ភ
	2887	FPOHO! DPA		2 6	3000	GEEDDHOLDBAEGA	20	_ σ	45
: E	2888	FPHC! AFSY	9 2	, o	3034	RRAFPHCI AFSYMOD	527	, <u>-</u>	ני
d d	2889	FRKIPMGVG	9 4	0 8	3036	II GEBKIPAGVGI SP	40.8) (C
g d	2890	FRKLPVNRP	91	80	3037	KOCFEKI PVNRPIDW	616		45
×	2891	FSSAGPCAL	19	56	3038	VCAFSSAGPCALRFT	09	81	06
₩	2892	FSWLSLLVP	20	100	3039	SVRFSWLSLLVPFVQ	330	16	80
ğ	2893	FTFSPTYKA	19	95	3040	KQAFTFSPTYKAFLC	653	12	09
ಕ್ಷ	2894	FTGLYSSTV	18	06	3041	VGNFTGLYSSTVPVF	56	Ξ	55
젒	2895	FTSAICSVV	19	95	3042	LAOFTSAICSVVRRA	515	19	98
PN N	2896	FVGLSPTVW	19	95	3043	VQWFVGLSPTVMLSV	343	14	20
×	2897	PAGGGRHK	18	06	3044	LKVFVLGGCRHKLVC	129	4	70
8	2898	FVOWFVGLS	19	98	3045	LVPFVQWFVGLSPTV	339	19	98
≅	2899	FVYVPSALN	18	06	3046	GTSFVYVPSALNPAD	763	16	80
ರ್ಷ	2900	IDWKVCQRI	17	82	3047	NRPIDWKVCQRIVGL	614	16	80
2 66 €	2901	IFLFILLC	91	80	3048	RFIIFLELCLIF	242	.	7.5
}	2902	FLLVLLDY	5 ·	S (3049	CCIFCLVLLDYOGM	252	6.	S (
z :	2903	IGTDINSVAL	9 !	080	3050	AKLIGTONSVVLSHK	731	5.	65
로 :	2904	IHTAELLAA	17	90	3051	PLPIHTAELLAACFA	711	9 ,	08 7
<u> </u>	2905	IIFLFILL	9 :	င္ဆ	3052	RRFIIFLECLI	241	15	75
≱	2906	ILLCUFL	20	100	3053	FLFILLCUFILVL	246	9 :	80
Z :	2907	LAGISEVY	16	08	3054	ANWILHGTSFVYVPS	757	9 9	0 0 0
3 2	2908	LSILPEII	0.7	001	3055	NAPILSTLPETTVM	165	<u> </u>	o .
} 	6067	IPIPSSWAF	0 9	3 5	3056	CICIFICOSWAFAHF	321	» ;	a 6
₹ 8	2011	LANCEABOD		n u	3057	GVWIRITHATHTRA *G:- **Onvocoon	123		n (
2 8	2012	1 AECVADOV		0 0	0000	PLO AECVADOVA O	111	2 9	0 0
<u> </u>	2012	I AOETSAIC	2 2	מי	6000	PELL ADETSAICSWV	- 6	9 9	9 4
	2914	WEW WE'D	17	2.5	3064	ASKI CI GWI WGMDID	1 0	2 2	9 6
} ≥	2915	N I BI DI		50,	3062	III CHELIVII DY	240) v
: : ×	2916	I CI BPVGAF	9 5	9.5	3005	RDM CL RPVGAFSRG		2 5	9 0
. Z	2917	LCOVEADAT	. .		3064	RPGLCOVFADATPTG	089	: =	20.00
№	2918	LDSWWTSLN	61	96	3065	POSLDSWWTSLNFLG	192	17	8 8
2	2919	LDTASALYR	17	85	3066	RDLLDTASALYREAL	28	16	80
절	2920	LDVSAAFYH	19	95	3067	WLSLDVSAAFYHIPL	425	Ξ	55
₩	2921	LDYGGMLPV	18	90	3068	LVLLDYQGMLPVCPL	258	18	06
ಕ	2922	LEEELPRLA	18	06	3069	AGPLEEEL PRLADEG	18	. 13	65
8	2923	LFILLICLI	91	08	3070	IIFLFILLICLIFIL	244	16	80

HBV DR-SUPER MOTIF

Table XIXa

Protein	Core SEQ ID NO:	Core · Sequence	Core Freq.	Core Conservancy (%)	Exemplary SEQ ID NO:	Exemplary Sequence	Position In HBV Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ಕ	2924	LGAKSVOHL	17	85	3071	DVVLGAKSVQHLESL	541	16	80
ಕ	2925	LGFAAPFTQ	19	95	3072	VGLLGFAAPFTQCGY	626	19	95
ಜ	2926	LGFRKIPMG	19	98	3073	PIILGFRKIPMGVGL	496	13	65
ಕ	2927	LGNUNSIP	19	95	3074	DLNLGNLNVSIPWTH	40	19	95
%	2928	LGPLLVLOA	19	95	3075	SGFLGPLLVLQAGFF	169	15	7.5
z ?	2929	LHPAAMPHL	20	00.	3076	HLPLHPAAMPHLLVG	425	o '	45
& 8	2930	LIFILACLD	6 ·		3077	LICUFILVILDYOG	. 251	6 -	50.0
₫,	1883	LKLIMPARF	3.5	ر د ا	3078	KHRIKLIMPAHFYPN	104	, ,	e S
۷ د	2832	LAVEVIGGE 11 AOETSAI	<u>.</u>	, s	3079	EIFLAVFVLGGCHHA Speil Anstrainesv	126	e •	
3 3	2934	LLDTASALY		25.00	3081	STELEGIE SAUSK IRDLLOTASALYREA	9.5	<u>n</u> o	9. 4. C. 7.
భ	2935	LLGCAANWI	91	80	3082	FPWLLGCAANWILRG	749	. 5	7.5
್ದ	2936	LLGFAAPFT	19	95	3083	IVGLLGFAAPFTOCG	625	81	06
%	2937	LIGWSPOAD	17	85	3084	HGGLLGWSPQAQGIL	09	15	7.5
₩ A	2938	LLCUFIL	20	100	3085	LFILLLCLIFILVLL	247	16	80
SE SE	2939	LLSFLPSDF	19	98	3086	SVELLSFLPSDFFPS	41	=	55
⊉ :	2940	LISLGIHLN	19	98	3087	TNFLLSLGIHLNPNK	260	15	75
ğ ;	2941	LLSSNLSWL	89	06	3088	LTNLLSSNLSWLSLD	404	18	06
2	2942	LLTRILTIP	16	80	3089	GFFLLTRILTIPOSL	181	16	80
≥ i	2943	LLVLOAGFF	19	95	3090	LGPLLVLQAGFFLLT	172	@ :	06
§ :	2944	LVPFVOWF	50	100	3091	WLSILVPFVQWFVGL	335	6	95
⊋ 8	2945	LWFHISC	æ (06	3092	HOLLWHISCLIFG	126	e :	92
₹ 8	2946	LIMPLYACIO	D (ກ ເ	3093	YPALMPLYACIOSKO	640	= :	52
₹ 8	2947	LNLGNLNVS			3094	AEDLALGALINVSIPW	38	<u></u>	36
₹ 8	2948	LNPNKIKHW	2 !	5.2	3095	GIHLUPNKTKHWGYS	567	÷.	75
₹ 8	6667	UNFHVAEUL		ກີ	3096	DEGLINHHVAEDUNEG	9.0	2 5	09
Z	2950	LNVS/PWIR	D C		3097	LGNLNVSIPWIPKVG	460	5	ഹ ദ
3 ≥	2952	I PIFFC! WV	90	50	3000	LSTLFETTVANGAR	376	5 6	9 9
i g	2953	LPIHTAELL	17	85	3100	VAPLPHTAELLAAC	502) o	. 25
<u>්</u> ද	2954	LPVNRPIDW	19	90	3101	FRKLPVNRPIDWKVC	809	51	75
ಶ	2955	LOFFNSKPC	18	06	3102	CWWLQFRNSKPCSDY	312	10	20
×	2956	LAGLPVCAF	. 19	95	3103	HLSLRGLPVCAFSSA	52	18	06
×	2957	LRPVGAESR	18	06	3104	VLCLRPVGAESRGRP	15	18	06
2	2958	LROALCWG	18	06	3105	HTALROAILCWGELM	52	18	06
%	2959	LARFIIRE	15	7.5	3106	WMCLRRFIIFLFILL	237	15	75
3 8	2960	LSHPSOF	6 9	500	3107	VELLSFLPSOFFPS	42	0 :	20
₹ 8	1962	LSLDVSAAF	6.0	95	3108	LSWLSLDVSAAFYHI	423	<u> </u>	52
} ;	7967	LSCENFING	07	<u> </u>	3109	FSWLSLLVFFVCWFV	333	5	ກ (
٤ ۲	2963	CSCHOLLYC	D (ກ ເ	3110	GAHLSLKGLPVCA-S	50	æ ç	06
로 :	2964	LSPILLAGE	6	S	3111	GVGLSPFLLAQFTSA	207	9 .	80
₹ 8	2965	LSHKYTSFP	17	500	3112	SWLSRKY1SFPWLL	739		82
₹ ;	2966	LSSNLSWLS	20 :	0.5	3113	INLLSSNLSWLSLDV	405	8	06
≩ 8	2967	LSVPNPLGF	15	75	3114	GINLSVPNPLGFFPD	13	4 (70
₹ 8	2362	LSWLSLDVS	0,7	2 5	3115	SSNLSWLSLDVSAAF	204	2 ;	
Š 6	6067	CILCACIOS	<u>.</u>	0 0	3116	I FILL I PUSE DSWWI	981	<u></u>	ري
걸 중	2970	LINELSSNE	20 Y	0 0	3117	LOSE I NILLSSNESWE	401	20 L	0.6
ž (- /87		<u> </u>	200	3118	FFLLIPUSED	182	<u>.</u>	
4	2972	LVDKNFHNI	07,	00.0	3119	GVFLVDKNPHNIJES	372	= ;	55
3	5/67	LVS-GVWIH	<u>0</u>	⊃ m ·	3120	LEYLVSFGVWIHIPP	145	7	0/

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Table XIXa

Protein	Core SEQ ID NO:	Core Sequence	Core Freq.	Core Conservancy (%)	Exemplary SEQ ID NO:	Exemplary Sequence	Position In HBV Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ğ	2974	LWDFSOFS	20	100	3121	ESPLVVDFSOFSBGN	374	6	45
2	2975	LWFHISCLT	17	85	3122	ROLLWFHISOLTFGR	86	17	85
3	2976	LWGMDIDPY	17	85	3123	LGWLWGMDIDPYKEF	24	17	85
젒	2977	LWKAGILYK	20	100	3124	LHTLWKAGILYKRET	148	18	06
2	2978	LYREALESP	17	85	3125	ASALYREALESPEHC	34	17	85
	2979	LYSHPIILG	16	90	3126	KLHLYSHPIILGFRK	489	16	80
ೱ	2980	MDDVVLGAK	18	06	3127	FSYMDDVVLGAKSVQ	536	18	06
ಕ್ಷ	2981	MGVGLSPFL	16	80	3128	KIPMGVGLSPFLLAQ	503	16	80
젙	2982	MPHLLVGSS	17	85	3129	PAAMPHLLVGSSGLS	430	80	40
№	2983	MOWNSTIFH	16	80	3130	POAMOWNSTTFHOTI.	106	œ	40
×	2984	MSTTDLEAY	15	7.5	3131	LSAMSTTDLEAYFKD	100	O	45
8	2985	MWYWGPSLY	17	85	3132	IWMMWYWGPSLYNIL	369	6	45
×	2986	VCAFSSAGP	19	95	3133	GLPVCAFSSAGPCAL	57	18	06
젍	2987	VCCRIVGIL	17	85	3134	DWKVCQRIVGLLGFA	618	17	85
<u>ಕ</u>	2988	VFADATPTG	19	92	3135	LCQVFADATPTGWGL	683	19	98
&	2989	VGLSPTVWL	19	95	3136	QWFVGLSPTVWLSVI	344	14	7.0
전	2990	VGPLTVNEK	17	85	3137	QQYVGPLTVNEKRRL	93	80	40
ೱ	2991	VHFASPLHV	16	80	3138	PDRVHFASPLHVAWR	816	12	9
×	2992	VLCLRPVGA	19	95	3139	ARDVLCLRPVGAESR	12	4-	70
ಶ	2993	VLGAKSVQH	19	92	3140	DDVVLGAKSVQHLES	540	16	80
×	2994	VLHKRTLGL.	17	82	3141	LPKVLHKRTLGLSAM	68	= :	55
헕 :	2995	VPNLOSLTN	6 :	36	3142	KFAVPNLOSLINLLS	395	3	S 0
3	2996	VOASKLCLG	9-	80	3143	CPTVQASKLCLGWLW	14	5	75
8	2997	VRFSWLSLL	9 1	80	3144	WASVRFSWLSLLVPF	328	13	65
<u>ಕ</u>	2998	VARAFPHCL	0	95	3145	CSVVRRAFPHCLAFS	523	<u>6</u>	S (
<u>ದ</u> :	2999	VSIPWTHKV	20	100	3146	NLNVSIPWTHKVGNF	45	6 9	95
2	3000	VWIRTPPAY	<u>6</u> :	95	3147	SFGVWIRTPPAYRPP	121	80 (06
ಕ್ಷ	3001	VYVPSALNP	æ :	06	3148	TSFVYVPSALNPADD	764	9	80
3	3002	WFHISCLTF	©	06	3149	OLLWFHISCLIFGRE	66	17	82
%	3003	WFVGLSPTV	6-	95	3150	FVQWFVGLSPTVMLS	342	6	50
ಕ್ಷ	3004	WILRGTSFV	9-	80	3151	AANWILRGTSFVYVP	756	4	70
2	3005	WIRTPPAYR	6-	95	3152	FGVWIRTPPAYRPPN	122	6	90
ઇ 8	3006	WKAGILYKH	20	00 t	3153	HILWKAGILYKHEII	94.	æ ;))
로 1	3007	WLLGCAANW	9 9	08	3154	SFPWLLGCAANWILH	847	٠ ت	7.5
₹ 8	3008	WLSLDVSAA	n (66,	3155	NLOWLULDVOARTT		- 0	, a
£ 8	3008	WESTLVPFV	0.7	00 c	3156	HESWLEILVIFFOUNT	332	0.7	2 :
뒫	3010	WPKFAVPNL	<u>.</u>		3157	HVSWPKFAVPNLCSL	0.60	= ;	200
₹ 8	3011	YMUUVVLGA	æ ;	000	3158	AFSYMDDVVLGAKSV	535	8 9	
걸 ;	3012	YPALMPLYA	5.	r (3159	CCGYPALMPLYACIO	63/	6	G 6
≥ 1	3013	YCEMLPVCP	20 1	0.4	3160	LLDYGGMLPVCPLIP	260	0.	20
2	3014	YRPPNAPIL	50	100	3161	PPAYRPPNAPILSTL	129	<u>6</u>	56
%	3015	YRWMCLRRF	6-	95	3162	CPGYRWMCLRRFIIF	232	6-	95
ಕ್ಷ	3016	YSHPIILGF	16	08 .	3163	LHLYSHPIILGFRKI	490	91	80
젙	3017	YSLNFMGYV	15	75	3164	RWGYSLNFMGYVIGS	588	Ξ	55
ರ್	3018	YVPSALNPA	2	06	3165	SFVYVPSALNPADDP	765	16	80
№	3019	FFCLWY1Z	20				382		
2	3020	MGTNLSVPN	15				12		

HBV DR-SUPER MOTIF With Binding Data

Table XIXB

Drw53	0.0180			0.0150	0	2.6000			0.1600		0.0010	
DR9			1.3000	0.0250	0.5400	2.5000	0.3400			0.0450	0.0590	
DR8W2			0.2600	0.0580	0.1200	0.6600	0.0610			0.5300	0.0580	
DR7	0.0008	0.0018	3.1000	0.4000	0.3300	0.0092	0.2700	0.0003	0.0005	0.2200	0.0770 0.0013 0.0047	0.00770
DR6w19			0.3700	0.0043	0.0200	0.0018	0.0001			-0.0004	0.0800	
DR5w12			0.0700	0.0013	0.0024	0.6600	-0.0001			0.0140	0.0016	
· DR5w11	0.0002	٠	3.6000	0.0130	0.2400	0.3800	0.0470		-0.0002	0.4800	0.0120 -0.0002 0.0018	
DR4w15	0.2800		0.1500	0.8500	0.2200	1.4000	0.4100			0.5700	0.1200	
DR4w4	0.0023	0.0041	5.3000	1.2000	1.1000 0.0140	0.1500	0.3800	0.0490	-0.0007	3.4000	0.0800 0.0017 0.0320	0.0092
DR3			0.0040	90000-	0.0090	0.0013	90000-			0.0120	-0.0013	0.0022
DRZwzß2	0.0013		0.0190	0.0210	0.1400	0.0140	0.0500		0.0009	7.2000	0.0042 -0.0005 0.0069	
DR2w281			0.0420	0.0022	0.2400	0.6900	0.0140			0.0420	0.0270	
OR1	0.0007	0.0005	4.6000	1.5000	0.5300	0.0130	0.3500	0.0046	0.0009	0.3700	0.1800 • 0.0002 0.0026	0.0034
Exemplary Sequence	LLGFAAPFTQCGYPA CQVFADATPTGWGLA WPKFAVPNLQSLTNL CLTFGRETVLEYUS PPSFGVFPSGSGEND	LIWENISCITEGRET MOLFHLCLIISCSCP FIFFILLCLIFLV FIFFILLCLIFL	AGFFLTRILTIPQS CLIFLLVLLDYGGML GLYFPAGGSSSGTVN LGFFDHQLDPAFGA RRAFPHCLAFSYMDD	ILGFRKIPMGVGLSP KQCFRKLPVNRPIDW VCAFSSAGPCALRFT	SVRFSWLSLLVFFVQ KQAFTFSPTYKAFLC VGNFTGLYSSTVPVF	VQWFVGLSPTVWLSV LKVFVLGGCRHKLVC LVPFVQWFVGLSPTV	GTSFVYVPSALNPAD NRPIDWKVCQRIVGL RFIIFLFILLCLIF	AKLIGTONSVULSRK PLPIHTAELLAACFA RRFIIFLFILLLCLI FLFILLCLIFLLVL	ANWILRGTSFVYVPS NAPILSTLPETTVVR CTCIPIPSSWAFARF	GVWIRTPPAYRPNA AELLAACFARSRSGA PHCLAFSYMDDVVLG	PFLLAQFTSAICSVV ASKLCLGWLWGMDID ILLCLIFLLVLDY RDVLCLRPVGAESRG RPGLCQYFADA FPTG	PUSLUSWWISLINFUS RDLLDTASALYREAL WLSLDVSAAFYHIPL LVLLDVQGMLPVCPL AGPLEEELPRLADEG IIFLFILLCLIFLL
SEO ID NO:	3021 3022 3023 3024	3026 3027 3028 3029	3031 3032 3033 3034 3035	3036 3037 3038	3040 3041 3041	3043 3045 3045	3046 3047 3048	3050 3051 3052 3053	3054 3055 3056	3057 3058 3059	3060 3061 3062 3063	3066 3067 3068 3069 3070
Core Sequence	FAAPFTQCG FADATPTGW FAVPNLQSL FGRETVLEY	FHISCLFG FHICLISC FILLCLIF FLFILLCL	FLLTRILTI FLLVLDYQ FPAGGSSSG FPOHOLOPA FPHCLAFSY	FRKIPMGVG FRKLPVNRP FSSAGPCAL	FTFSPTYKA FTGLYSSTV FTSAICSVV	FVGLSPTVW FVLGGCRHK FVQWFVGLS	FVYVPSALN IDWKVCQRI '	IGTONSVVL IHTAELLAA IIFLFILLL ILLCLIFL	ILRGTSFVY ILSTLPETT IPIPSSWAF	IRTPPAYRP LAACFARSR LAFSYMDDV	LAGPTSAIC LCLGWLWGM LCLIFLLVL LCLIFLVL LCLFVGAE LCQVFADAT	LDSWWISEN LDTASALYR LDVSAAFYH LDVGMLPV LEEELPRLA LFILLLCU
Core SEQ ID NO:	2874 2875 2876 2877	2879 2880 2881 2882 2883	2884 2885 2886 2886 2887	2889 2890 2891	2893 2894 2894 2895	2896 2897 2898	2899 2900 2901	2903 2904 2905 2906	2904 2908 2909	9910 2911 2912	2913 2915 2916 2917	2918 2920 2921 2922 2923

				HBV C	HBV DR-SUPER MOTIF With Binding Data	MOTIF	With B	inding D	ata					
Core SEQ ID Exemplary Sequence NO: Sequence		Exemplary Sequence	DB:	DR2w281	DR2w282	DFG	DR4w4	DR4w15	DR5w11	DR5w12	DR6w19	DR7	DR8w2 DR9	DRw53
3071		OVVLGAKSVQHLESL /GLLGFAAPFTQCGY	0.0470	0.3100	0.0008		-0.0014		-0.0004	•	-0.0001	0.0014	0.5700	
LGFHAIFMG 3073 FILLGFHAIPMGVGL LGAILNVSIP 3074 DANLGAILNVSIPWTH LGPI VI OA 3075 SGFLGPI VI OAGEF		SILGERALIPMONGL SINLGNILNVSIPWTH SIGH GPI VI OAGEF	0.0038				0.0240					0.0010		
3076		1.PLHPAAMPHLLVG												
		KRRLKLIMPARFYPN FIRI KVPM GGCRHK												
3080		SPFLLAGFTSAICSV	0.1200	0.0200	0.0085	-0.0013	0.0740	0.0190	-0.0002	-0.0013 0.0540	0.0540	0.0330	0.0014 0.0380	0.2000
LLDTASALY 3081 IRDLLDTASALYREA LLGCAANWI: 3082 FPWLLGCAANWILRG		RDLLDTASALYREA FPWLLGCAANWILRG												
3083		VGLLGFAAPFTQCG	0.0200		-0.0005		-0.0007		-0.0002			0.0009		0.0067
LLGWSFOAD 3084 HGGLEGWSFOADGIL LLLCLIFL 3085 LFILLLCLIFLLVLL		-IGGILGWSPOAGGIL -FILLICLIFILVIL												
3086		SVELLSFLPSDFFPS												
LESCHEN 3087 INFLESCENTINENT 11 SSNI SWI SLD		INFLESTGIFFLAPAK Thi i SSNI SWI SI D	3.5000	0.0410	0.1200		0.0220	0.0360	0.0053	-	0.0160	0.2200	0.0032 0.3800	-
3089		SFELTRILTIPOSL	0.4300	0.0150	0.0110		3.1000	0.4500	2.3000		0.0780	3.5000	1.6000 0.5500	
3090		-GPLIVLOAGFFLLT												
LVPFVCWP 3091 WLSLLVPFVCWFVGL LLWFHISCL 3092 IROLLWFHISCLTFG		MLSLLVPFVOWFVGL ROLLWFHISOLTFG												
LMPLYACIQ 3093 YPALMPLYACIQSKQ	YPALMPLYACIOSKO	~	0.2400		4000		0.0014		0			0.0011		
3095	-	SIHLNPNKTKRWGYS	0.000.0		-0.0003		-0.000		-0.0002		•	0.000		0.0170
3096		DEGLINPRIVAEDLINI.G												
LNVSIPWTH 3097 LGNLNVSIPWTHKVG		STIPMINK SPACE												
3099		PLLPIFFCLWWYIZ												
3100	-	VAPLPIHTAELLAAC												
LPVNRPIDW 3101 FRKLPVNRPIDWKVC 10FRVSKPC 3102 CWM OFRVSKPCSDY		FRKLPVNRPIDWKVC												
3103		HLSLRGLPVCAFSSA	1.3000				0.0028					0.0130		
3105		HTALROALCWGELM												
3106	-	WMCLRRFIIFLFILL										٠		
CSPLYSUPP 310/ VELLSPLYSUPPS/		VELLSPLPSDPPPSI												
3109		FSWLSLLVPFVQWFV												
3110		GAHLSLRGLPVCAFS	0.7800		0.0042	-0.0041	0.0011		0.0025			0.0077		0.0150
LSPELLAUF 3111 GVGLSPFLLAUFISA SRKYTSFP 3112 SVVLSRKYTSFPWIL		GVGLSPFLLAGFISA SVVLSRKYTSFPWL	0.0005		0 0057	0 2 1 0 0	-0.0016		0.5300			0.030		
3113		TNLLSSNLSWLSLDV	0.0016		-0.0005	2	0.1300		0.0006			0.0019		0.0410
3114		GTNLSVPNPLGFFPD												
SWLSLDVS 3115 SSNLSWLSLDVSAAF		SSNLSWLSLDVSAAF	0.1400	0.0030	-0.0005	1.5000	0.2700		0.0046	0.0180	0.1000	0.0039	0.0460 0.0110	6.2000
3117	_	LOSL TNLL SSNL SWL	2.5000	0.4400	0.0200	-0.0013	4.8000	0.8100	0.0680	0.7500	0.0260	0.1500	0.0880 0.1100	
LTRILTIPO 3118 FFLLTRILTIPOSLD		FFLLTRILTIPOSLD												
3120	_	LEYLVSFGVWIRTPP												

	DRw53	0.0096	0.0130		0.0460	0.0009	0.0044	2.4000 0.0031 -0.0005	0.0015	
	DR9			0.2400	0.0056	0.0800	0.2700	0.0620		0.0490
•	DR8w2	0.0029		0.0035	0.0250		0.2500	0.0150		0.0610 0.0490
	DR7	-0.0014 0.0061 0.0004	0.1200	0.0810	-0.0003	0.0005	0.5800	0.0041 0.0005	0.0006	0.0006
	DR6w19	0.0040		0.0190	0.0088	0.0002	0.0250	0.0330		0.0002
	DR5w12				-0.0013		0.3700	0.0022		0.0310
ata	DR5w11 [-0.0004 0.0011 -0.0002	0.2500	0.0008			0.0072	0.0033	0.0023	0.0410
inding D	DR4w15	·	·	0.0054	-0.0022	0.0630	0.0250			0.1600
With B	DR4w4	0.0140	0.030	0.0008	0.1300	-0.0007 0.0780	0.0130 0.0510	0.2900 -0.0007 2.9000	0.0068	0.6800
MOTIF	82	2.6000			0.0032	-0.0041 -0.0009	0.0023	1.3000		0.0040
DR-SUPER MOTIF With Binding Data	DR2w282	-0.0010 0.0009 0.0006	-0.0026	0.0008	-0.0003	-0.0005 0.4300	0.0160	-0.0005 0.0009 -0.0005	0.0018	0.0400
HBV D	DR2w281	0.0074		0.0290	0.0005	0.0110	0.0035 0.0240	0.0003		0.0340
	DRI	0.0007 0.0002 0.0004	0.0012	0.0510	0.0180	0.0001	0.0920	0.1400 0.0430 0.0027	0.0062	0.0220
	Exemplary Sequence	ESPLVDFSØFSRON ROLLWFHISOLTFGR LGWLWGMDIDPYKEF LHTLWKAGILYKRET ASALYREALESPEHC KLHLYSHPIILGFRK FSYMDDVALGAKSVO KIPMGVGLSPFLLAO	PAAMPHLLVGSSGLS POAMOWNSTTFHOTL LSAMSTTOLEAYFKD IMMAMWYWGPSLYNIL GLPVCAFSSAGPCAL DWKVCORIVGLLGFA LCOVFADATPTGWGL	Owfvglsptvm.svi Ooyvgpltvnekarl Pdrvhfasplhvawr Ardvlclapvgaesr Ddvvlgaxsvohles Lpkvlhkrtglsam	KFAVPNLOSLTNLLS CPTVOASKLCLGWLW WASVRFSWLSLVPF CSVVRRAFPHCLAFS	NLNVSIPWTHKVGNF SFGVWIRTPPAYRPP TSFVYVPSALNPADD QLLWFHISCLTFGRE	FVQWFVGLSPTVMLS AANWILRGTSFVYVP FGVWIRTPPAYRPPN HTLWKAGILYKRETT SFPWLLGCAANWILR	NI.SWLSLDVSAAFYH RFSWLSLLVPFVGWF RVSWPKFAVPNLGSL AFSYMDDVVLGAKSV	OCGYPALMPLYACIO LLDYOGMLPVCPLIP PPAYRPPNAPILSTL CPGYRWACI RREIIF	LHLYSHPII(GFRKI RWGYSLNFWGYVIGS SFVYVPSALNPADDP
	SEQ ID		3129 3130 3132 3132 3134	3136 3137 3138 3140	3142 3143 3144 3145	3146 3147 3148 3149	3150 3151 3152 3153	3155 3156 3157 3158	3159 3160 3161	3163 3164 3165
	Core Sequence	LVVDFSQFS LWFHISCLT LWGMDIDPY LWGMDIDPY LWAGGLYK LYREALESP LYSHPIILG MDDVVLGAK MGVGLSPFL	MPHLLVGSS MOWNSTTFH MSTTDLEAY MWYWGPSLY VCAFSSAGP VCAFSSAGE VCAFSSAGE	VGLSPTVML VGPLTVNEK VHFASPLHV VLCLRPVGA VLGAKSVQH VLGAKSVQH	VPNLQSLTN VQASKLCLG VRFSWLSLL VRRAFPHCL	VSIPWTHKV VWIRTPPAY VYVPSALNP WFHISCLTF	WFVGLSPTV WILRGTSFV WIRTPPAYR WKAGILYKR WLGCAANW	WLSLDVSAA WLSLLVPFV WPKFAVPNL YMDDVVLGA	YPALMPLYA YQGMLPVCP YRPPNAPIL	YSHPIILGF YSLNFMGYV YVPSALNPA FFCLWYYIZ MGTNLSVPN
Table XIXB	Core SEQ ID NO:	2974 2975 2976 2977 2978 2980 2980	2982 2983 2984 2985 2986 2987 2988	2989 2990 2991 2992 2993	2995 2996 2997 2998	2999 3000 3001	3003 3004 3005 3006	3008 3009 3010	3012 3013 3014	3016 3017 3018 3019 3020

Table XXa

Exemplary Sequence Conservancy (%)	95	75	75	100	80	06	100	95	100	85	85	100	95	95	00
Exemplary Sequence Frequency	6	14	9	11	13	13	20	11	თ	17	6	17	19	18	•
Position In Poly-Protein	10	136	241	360	731		120	412	374	34	27	34	683	256	535
Exemplary Sequence	PLGFFPOHOLDPAFG	CLIFGRETVLEYLVS	PRSFGVEPSGSGHID	GGVFLVDKNPHNTTE	AKLIGTDNSVVLSRK	AGPLEEELPRLADEG	TKYLPLDKGIKPYYP	LSWLSLDVSAAFYHI	ESPLWDFSQFSPGN	ASALYREALESPEHC	LWGMDIDPYKEFGAS	NRRVAEDLNLGNLNV	LCQVFADATPTGWGL	FLLVLLDYQGMLPVC	ACCVIDENCE OF ACCV
Exemplary SEQ ID NO:	3181	3182	3183	3184	3185	3186	3187	3188	3189	3190	3191	3192	3193	3194	3405
Conservancy (%)	95	75	7.5	100	80	90	100	95	100	95	82	100	95	95	c
Core Freq.	19	15	15	20	16	18	50	19	50	17	17	50	61	19	•
Core Sequence	FFPDHOLDP	FGRETVLEY	FGVEPSCSC	FLVDKNPHN	IGTDNSWL	LEEELPRILA	LPLDKGIKP	LSLDVSAAF	LWDFSQFS	LYREALESP	MOIDPYNEF	VAEDLNLGN	VFADATPTG	VLLDYOGML	AS IVVIOUS
Core SEO ID NO:	3166	3167	3168	3169	3170	3171	3172	3173	3174	3175	3176	3177	3178	3179	2100
Protein	ENV	NC	젛	젍	ర్జ	ర్జ	절	ర్డ	젍	3	3	전	젍	EN	Ē

HCV DR 3A Motif

DRW53															-0.0005
OR9															
DR8W2									0.0029						
DR7									-0.0014				0.0013		0.0003
DRSw12 DR6w19									0.4000				_		•
DR5w11		ŀ							-0.0004						0.0006
DR4w15															
DR4w4													0.9600		2.9000
DR3				0.0790		0.0022	-0.0017		2.6000			0.1400		0.0170	0.0130
DR2w2B2									-0.0010						-0.0005
DR2w281 DR2w282									0.0074						
DR1									0.0007				0.0020		0.0027
Exemplary Sequence	PLGFFPOHOLDPAFG	CLTFGRETVLEYLVS	PRSFGVEPSGSGHD	GGVFLVDKNPHINTTE	AKLIGTDNSVVLSRK	AGPLEEELPRLADEG	TKYLPLDKGIKPYYP	LSWLSLDVSAAFYHI	ESPLWDFSQFSPGN	ASALYREALESPEHC	LWGMDIDPYYEFGAS	NARVAEDLNLGNLNV	LCOVFADATPTGWGL	FLIVILDYOGMLPVC	AFSYMDDVVLGAKSV
SEQ ID NO:	3181	3182	3183	3184	3185	3186	3187	3188	3189	3190	3191	3192	3193	3194	3195
Core Sequence	FFPOHOLDP	FGRETMEY	FOMPSGSG	FLVDKNPHN	IGTONSVVL	LEEELPRIA	LPLDKGIKP	LSLDVSAAF	LVVDFSQFS	LYREALESP	MOIDPYNGF	VAEDLNLGN	VFADATPTG	VLLDYOGML	YMDDVVLGA
Core SEO ID NO:	3166	3167	3168	3169	3170	3171	3172	3173	3174	3175	3176	3177	3178	3179	3180

Table XXb

otein	Core SEQ ID NO:	Core Sequence	Core Freq.	Conservancy (%)	SEQ ID NO:	Exemplary Sequence	Position In HBV Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence	8.5
	3196	AHISHBGIP	œ	o	2006	STORY TO THE STORY TO	97	0	00 00	
ಕ	3197	FSPTYKAFL	9 9	9 4F 6 6F	3203	AFTESPTYKAFI CKO	655	• :	90.00	
ಕ	3198	IPWTHKVGN	50	100	3204	NVSIPWTHKVGNFTG	47	20	100.00	
ಕ	3199	LTVNEKRRL	17	85	3205	VGPLTVNEKRRLKLI	96	12	00.09	
×	3200	VGAESHGRP	19	95	3206	LPPVGAESPGRPVSG		. ~	35.00	
ಕ	3201	WLSRKYTS	18	06	3207	DNSVVLSRKYTSFPW	737	17	85.00	

HBV DR-3B Motif With Binding Information

Table XXd

82	
DRw53	1
DR3	
DR8w2	0.0092
0R7	-0.0014
DR6w19	0.0009
DR5w12	
DR5w11	0.0030
DR4w15	
DR4w4	·
DR3	0.0035 2.2000 -0.0017
DR2w2B2	0.0047
DR2w2B1	0.0022
DR1	0.0006
Exemplary Sequence	DHGAHLSIAGLPVCA AFTESPTYKAFLCKO NVSIPWTHVCKOFTG VGPLTVNEGRBLKU LPPVCAESRGPVSG DNSVVLSRKYTSFPW
SEO ID NO:	3202 3203 3204 3205 3206
Core Sequence (AHLSLAGLP FSPTYKAFL IPWTHKYGN LTYNEKRRL VGAESRGPP VVLSRKYTS
Core SEO ID NO:	3196 3197 3198 3199 3200 3201

TABLE XXI. Population coverage with combined HLA Supertypes

PHENOTYPIC FREQUENCY Caucasian North Japanese Hispanic Chinese Average **HLA-SUPERTYPES** American Black a. Individual Supertypes 45.8 A2 39.0 42.4 45.9 43.0 43.2 **A3** 37.5 42.1 45.8 52.7 43.1 44.2 **B**7 38.6 52.7 48.8 35.5 47.1 44.7 A1 47.1 16.1 21.8 14.7 26.3 25.2 A24 23.9 38.9 58.6 40.1 38.3 40.0 B44 43.0 42.9 21.2 39.1 39.0 37.0 **B27** 28.4 26.1 13.3 13.9 35.3 23.4 B62 12.6 4.8 25.4 36.5 11.1 18.1 B58 10.0 25.1 1.6 9.0 5.9 10.3 b. Combined Supertypes A2, A3, B7 83.0 86.1 87.5 88.4 86.3 86.2 A2, A3, B7, A24, B44, A1 99.5 98.1 100.0 99.5 99.4 99.3 A2, A3, B7, A24, B44, A1, 99.9 99.6 100.0 99.8 99.9 99.8 B27, B62, B58

SF 184895 v1

Table XXII	ХІІ			HBV	HBV ANALOGS					
¥ ¥	Sequence	Fixed Nomen.	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	. 1° Anchor Fixer	Analog	SEQ ID NO:
10	CILLCLIFL		z	>	z	z	z	2	A	3208
6	RMTGGVFLV	VM2.V9	z	>-	z	z	Z	-	: «	3209
6	LMPFVQWFV	VM2.V9	z	>	z	z	z	-	4	3210
တ	RLTGGVRLV	VL2.V9	Z	>-	z	z	z	-	∢	3211
თ	GLCQVFADV	L2.AV9	Z	>	z	z	z	-	∢	3212
o	WLRGTSFV	IL2.V9	Z	>-	z	z	Z	-	∢	3213
o	NLGNLNVSV	L2.IV9	zi	>-	Z:	Z	Z	-	4	3214
on c	YLPSALNPV	VL2.AV9	2 2	> :	z:	z	z:	- ·	∢	3215
, a	GEWINI PPV BI SWIDKENN	VL2.AV9	zz	> >	Z 2	zz	2 2	- ,	∢ ∙	3216
n or	I GI GEAV	VL2.43	: 2	≻ >	2 2	2 2	2 2	- •	∢ •	3210
) O	BMLTIPOSV	IM2.1 V9	z	- >	2 2	z z	2 2		∢	3210
6	SLDSWMTSV	L2.LV9	z	- >	: z	z	: z		< <	3220
10	FMLLLCLIFL	IM2.L10	z	· > -	z	: > -	z	• •-	(∢	3221
10	LMLQAGFFLV	VM2.LV	z	· > -	z	z	z	-	< ∢	3222
10	SMLSPFLPLV	IM2.LV1	z	>	Z	z	z	-	: ∢	3223
10	LMLLDYQGMV	VM2.LV	z	>-	z	z	Z	-	< <	3224
10	FLGLSPTVWV	VL2.LV1	z	>-	z	z	z	-	<	3225
æ	FPAAMPHL	٠	z	z	z	z	>-		∢	3226
80	HPFAMPHL		Z	z	z	z	>		4	3227
.	HPAAMPHI		zi	z	z	z	>		۷	3228
∞ 0	FMFSPTYK		z	Z	> :	Z	Z:		∢	3229
x c	FVFSFLYK	9	2 2	Z:	> :	Z	z :		∢	3230
o n 0	FLLIMILIV	L2.IV9	2 2	> :	z :	zi	Z:	-	∢	3231
n c	ALMPLYACV	12.109	z 2	> :	z:	zi	z:	-	∢	3232
o n c	LLAUFISAV	LZ.1V9	zz	> :	z:	zi	Z:	-	∢	3233
n c	L ASETS!	VL2.V9	2 2	> - :	zi	2 2	zi	- ,	∢	3234
n c	Verson 2	LZ.AV9	2 2	- ;	zi	2 2	zi	- ,	∢ ·	3235
ာတ	KLFLYSHPI	5	: z	- >	2 2	2 2	z z	- 5	∢ <	3237
6	LLSSNLSWV	L2.LV9	z	· >-	: Z	z	z	?	(<	3238
6	FLLSLGIHV	L2.LV9	z	· > -	z	z	z		(∢	3239
6	MMWYWGPSV	M2.LV9	z.	>	z	z	z	-	. ∢	3240
6	VLQAGFFLV	L2.LV9	z	>	z	z	z	-	: ∢	3241
6	PLLPIFFCV	L2.LV9	z	>	z	z	z	-	: ∢	3242
6	FLPIFFCL		Z _.	>	z	z	z	2	<	3243
о	VLLDYGGMV	L2.LV9	Z	>	z	z	z	-	⋖	3244
o	YMFDVVLGA		z:	>-	Z	z	z	2	∢	3245
o (GLGWSPQV	L2.AV9	z:	>	z	z	z	-	∢	3246
න ර	FPAAMPHIL		z z	z	Z :	Z:	> :		∢	3247
o n (HPFAMPHLL	-	z	z	z	Z	> :		∢	3248
מ	HPAAMPHLI		z	z	Z	Z	>		∢	3249

Table XXII	П			HBV	HBV ANALOGS					
ΑΑ	Sequence	Fixed	A1 Motif	A2 Super	A3 Super	A24 Motif	B7 Super	. 1 °	Analog	SEQ ID
				Motif	Motif		Motif	Fixer	and the second second	į
6	FPVCAFSSA		z	z	z	z	۶		∢	3250
O	LPFCAFSSA		z	z	z	z	>		∢	3251
O	LPVCAFSSI		z	z	z	z	>		< <	3252
o	FPALMPLYA		z	z	z	z	>		∢	3253
တ	YPFLMPLYA		z	z	z	z	>		∢	3254
6	YPALMPLYI		z	z	z	z	>		∢	3255
တ	FPSRGRLGL		z	z	Z	z	>		∢	3256
6	DPFFGRLGL		z	z	z	z	>		∢	3257
6	DPSRGRLGI ·		z	z	z	z	>		∢	3258
თ	SMICSVVRR		z	z	>-	z	z		∢	3259
6	SVICSVVRR		z	z	>-	z	z		∢	3260
თ	KVGNFTGLK		z	z	>-	z	z		∢	3261
o			z	z	· >	z	z		∢	3262
o	WFFSQFSR		z	z	>	z	z		∢	3263
თ	SVNRPIDWK		Z:	z	>-	Z	Z		4	3264
6	TLWKAGILK		z:	z	>-	Z	z		∢	3265
თ	TLWKAGILR		Z:	z	>-	z	z		4	3266
თ	TMWKAGILY		>- :	z	>-	Z	z		∢	3267
o	TVWKAGILY		z:	Z	>-	Z	Z		∢	3268
o (RMYLHTLWK	•	zi	z	> :	zi	zi		∢	3269
5 7 (HVYLHILWK		2 2	Z:	> :	zi	zi		∢ -	32/0
o	SWIDSPLYR		2 2	zz	> >	Z 2	z 2		∢ •	3271
no	SVVIDATION		z	2 2	- >	2 Z	2 2		∢ <	3273
9 07	SAIXSVVRB		z	2 2	- >	: z	: 2		< ⊲	3274
6	LPVXAFSSA		z	z	Z	z	· > -		< ∢	3275
10	FLLAQFTSAV	L2.IV10	z	>	z	z	z	-	∶ ∢	3276
10	YLFTLWKAGI		z	>	z	z	z	2	· •	3277
10	YLLTLWKAGI		z	>	z	z	z	2	∢	3278
0	LFYGGMLPV		z	>	z	Z	z	2	∢	3279
9	LLLYGGMLPV		z	>-	z	z	z	2	∢	3280
0	LLVLQAGFFV	L2.LV10	Z	>	z	z	z	-	∢	3281
0	ILLICLIFLY	L2.LV10	z į	>	z	z	z	-	∢	3282
-10	FPFCLAFSYM		Z	z	z	z	>		∢	3283
10	FPHCLAFSYI		z	z	Z,	z	>		∢	3284
9	FPARVTGGVF		Z	z	z	z	>-		∢	3285
0	TPFRVTGGVF		z:	z	z	Z	>-		∢	3286
9	TPARVTGGVI		Z	z	z	Z	>-		∢	3287
2 :	FPCALRFTSA		z	z	Z	z	> :		∢	3288
<u> </u>	GPFALRFTSA		z 2	z	zz	Z 2	≻ ;		∢ •	3289
2 9	GPCALRFISI		z 2	z:	z	2 2	≻ :		⋖ -	3290
-	TRAAMTHIV		<u> </u>	Z	Z	Z	-		∢	3291

Table XXII	=			HBV A	ANALOGS					
ΑΑ	Sequence	Fixed	A .	A2	A3	A24	87	-	Analog	SEQID
		Nomen.	Motif	Super Motif	Super Motif	Motif	Super Motif	Anchor Fixer		Ö
-	нремрицу		z	z	z	z	\		A.	3292
10	HPAAMPHLLI		z	z	z	z			: «	3293
0	QMFTFSPTYK		z	z	>	z	z		: ∢	3294
10	QVFTFSPTYK		z	z	>	z	z		V	3295
0	TMWKAGILYK		z	z	>-	z	z		A	3296
10	TVWKAGILYK		z	z	>	z	z		A	3297
2	VMGGVFLVDK		z	z	>	z	z		¥	3298
10	WGGVFLVDK		z	z	>	Z	z		¥	3299
10	SMLPETTVVR ·		z	z	>	z	z		∢	3300
10	SVLPETTVVR		z	z	>	z	z		4	3301
0	TMPETTVVRR		z	z	>-	z	z		4	3302
10	TVPETTWAR		z	z	>	z	Z		∢	3303
10	HTLWKAGILK		z	z	>	z	z		4	3304
10	HTLWKAGILR		z	z	>	z	z		4	3305
10	HMLWKAGILY		>	z	>-	z	z		4	3306
9	HVLWKAGILY		z	z	>	Z	z		4	3307
10	GMDNSVVLSR		z	z	>	z	z		⋖	3308
10	GVDNSVVLSR		z	z	\	z	z		. Α	3309
10	GTFNSVVLSR		z	z	>-	z	z		⋖	3310
10	YMFDVVLGAK		z	z	>	z	z		⋖	3311
10	MMWYWGPSLK		z	z	>-	z	z		4	3312
10	MMWWMGPSLR		z	z	>	z	z		∢	3313
6	ILLLXLIFL		z	>	z	z	z		⋖	3314
თ	LLXUFL		z	>	z	z	z		∢	3315
o	LLXLIFLLV		z	>	z	z	z		⋖	3316
တ	PLLPIFFXL		z	>	z	z	z		⋖	3317
6	ALMPLYAXI		z	>	z	z	z		4	3318
თ	GLXQVFADA		z:	>	z	z	z		4	3319
O	HISXLTFGR		z:	z	>-	z	z		4	3320
თ	FVLGGXRHK		z:	z	>-	z	z		· «	3321
10	FILLLXLIFL		z:	>	z	Z	z		4	3322
0	ILLLXUFLL		z	>	z	z	z		∢	3323
10	reduction of the contract of t		z.	>	z	z	z		∢	3324
9	LLPIFFXLWV		z	>-	z	z	z		⋖	3325
9	OLLWFHISXL		z	>	z	z	z		⋖	3326
-	LLGXAANWIL		Z,	>	z	z	z		⋖	3327
10	TSAIXSVVRR		Z	z	>-	z	z		⋖	3328
10	GYRWMXLRRF		z	z	z	>-	z		⋖	3329
10	GPXALRFTSA		z	z	z	z	>-		⋖	3330
0	FPHXLAFSYM		z	z	z	Z	>		4	3331
Ξ	HMLWKAGILYK		z	z	>-	z	z		⋖	3332
Ξ	HVLWKAGILYK		z	z	>	z	z		⋖	3333

Table XXII	₽			HBV	HBV ANALOGS					
AA	Sequence	Fixed Nomen.	A1 Motif	A2 Super	A3 Super	A24 Motif	B7 Super	1 ° Anchor	Analog	SEQ IC
				Motif	Motif		Motif	Fixer		
=	SMLPETTVVRR		z	z	٨	z	z		A	3334
Ξ	SVLPETTVVRR		z	z	>	z	z		∢	3335
=	GMDNSVVLSRK		z	z	>	z	z		∢	3336
Ξ	GVDNSVVLSRK		z	z	>	z	z		∢	3337
Ξ	GTFNSVVLSRK		z	z	>	z	z		∢	3338
œ	MPLSYQHI		z	z	z	z	>		∢	3339
æ	LPIFFCLI		z	z	z	z	· >		∢	3340
80	SPFLLAQI		z	z	z	Z	>		∢	3341
80	YPALMPLI		z	z	Z	z	>		∢	3342
&	VPSALNPI		z	z	z	z	>		∢	3343
6	LPIFFCLWI		z	z	z	z	>		∢	3344
6	LPIHTAELI		z	z	z	z	>		∢	3345
10	VPFVQWFVGI		z	z	z	z	>		∢	3346
Ξ	NPLGFFPDHOI		z	z	z	z	>		∢	3347
-	LPIHTAELLAI		z	z	z	z	>		∢	3348
თ	FLPSYFPSA	L2.FY5.	z	>	z	z	z	Rev3	∢	3349
10	YLHTLWKAGV	L2.IV10	Z:	>	z	z	z	-	۷	3350
=	STLPETYWAR	•	Z :	z	>-	z	z		∢	3351
о	YMDDVVLGV	M2.AV9	z:	>	Z	Z	Z	-	∢	3352
o	FPIPSSWAF		z:	z	z	z :	> 1		∢	3353
ന (IPITSSWAF		z 2	Z	z	z	> :		∢	3354
თ (PILSSWAF	•	Z 2	z	z	2 2	> >		⋖ •	3355
o n 0	PPVCLAFSY		2 2	z:	zi	2 2	≻ >		∢ ·	3356
o n c	TENCLAFAY		z z	z;	zz	2 2	- >		∢ •	7325
ם מ	IPPOMENTE		z 2	zi	z 2	2 2	- >		۷ ۰	2220
n o	F I MOVE A		z	z 2	2 2	2 2	- >		. ≪ ≪	9360
, ¢	B PSZEFPSV		z	z >	2 2	2 2	- z	Ş	₹. <	3361
0	FLPSZFFPSV		z	- >	: 2	z	: Z	? 2	(⊲	3362
6	IPFPSSWAF		z	·z	z	z	: > -	!	(∢	3363
თ	IPIPSSWAI		z	z	z	z	>		: ∢	3364
6	FPFCLAFSY		z	z	z	z	>		< <	3365
თ	FPHCLAFSI		z.	z	z	z	>		∢	3366
თ	FPHCLAFSA		z	z	z	z	>		∢	3367
10	FQPSDYFPSV		z	>	z	Z	z	Rev	∢	3368
თ	YLLTRILTI		Z	>-	z	z	z		∢	3369
တ	FLYTRILTI	-	Z	>	z	z	z		∢	3370
တ	FLLTYILTI		Z i	>	z	z	Z		∢	3371
თ	FLLTRILYI		Z:	>	z	z	Z		4	3372
Ξ,	FLPSOFFPSVR		zi	z	> :	Z:	Z:		∢	3373
თ (FLPSOFFPS		zi	Z :	z	z	Z:		∢	3374
×	FLYSDFF		Z __	z	z	z	Z		∢	33/5

able XXII				HBV	HBV ANALOGS					
ΑΑ	Sequence	Fixed Nomen.	A 1 Motif	A2 Super	A3 Super	A24 Motif	B7 Super	1° Anchor	Analog	SEQ IC
			100	Motif	Motif		Motif	Fixer		
10	FLPSDFFPSI	L2.VI10	z	>	z	z	z	Rev	∢	3376
10	FLPSDYFPSV		z	>	z	z	z	2	¥	3377
12	YSFLPSDFFPSV		z	z	z	z	z		< <	3378
10	YNIMGLKFROL		z	z	z	z	z		<	3379
6	NMGLKYROL		z	>	z	>	z	2	< <	3380
10	FLPS(X)YFPSV		z	z	z	z	z		4	3381
10	FLPSD(X)FPSV		z	z	z	z	z		∢	3382
1	FLPSDLLPSVR		z	z	>-	Z	z		∢	3383
12	FLPSDFFPSVRD ·		z	z	z	z	z		. ∢	3384
12	LSFLPSDFFPSV		z	z	z	z	z		∢	3385
-	SFLPSDFFPSV		z	z	z	Ż	z		: ∢	3386
œ	PSDFFPSV		z	z	z	z	z		: ∢	3387
6	FLMSYFPSV		z	· >-	z	z	z	2	: ∢	3388
6	FLPSYFPSV	L2.FY5.	z	>	z	z	z	ო	: ∢	3389
0	FLMSDYFPSV		z	>	z	z	z	2	: ∢	3390
Ξ	CILLICUFIL	-	z	>	z	z	z	2	: ∢	3391
10	FLPNDFFPSA	L2.5N4.	z	>	z	z	z	Rev	: ∢	3392
10	FLPDDFFPSA	L2.SD4.	z	>	z	z	z	Rev	< <	3393
10	FLPNDFFPSV		z	>	z	z	z	2	< <	3394
10	FLPSDFFPSA	L2.VA10	z	>	z	z	Z	Rev	∢	3395
10	FLPDDFFPSV		z	>	z	z	z	2	∢	3396
10	FLPADFFPSV		z	>	z	z	Z	2	∢	3397
10	FLPVDFFPSV		z	>	z	z	Z	2	∢	3398
10	FLPADFFPSi	L2.SA4.	z	>	z	z	z	Rev	∢	3399
0	FLPVDFFPSI	L2.SV4.	z	>	z	z	Z	Rev	∢	3400
10	FLPSDAFPSV		z	>	z	z	Z	2	∢	3401
10	FLPSAFFPSV		z	>	z	z	Z	2	4	3402
0	FLPSDFAPSV		z	>	z	z	Z	2	∢	3403
10	FLPSDFFASV		z	>	z	z	z	2	∢	3404
10	FLPSDFFPAV		z	>	z	z	z	2	∢	3405
10	FLASDFFPSV		z	>	z	z	Z	2	∢	3406
0	FAPSDFFPSV	LA2.V10	z	>	z	z	z	Rev	∢	3407
0	ALPSDFFPSV		z.	>	z	z	Z	2	∢	3408
10	YLPSDFFPSV		Z	>	z	z	Z	2	< <	3409
10	FIMPSDFFPSV	LM2.V1	z	>	z	z	Z	-	∢	3410
10	FLKSDFFPSV		z	>	z	z	z	2	⋖	3411
10	FLPSEFFPSV		Z	>	z	z	z	2	⋖	3412
9	FLPSDFYPSV		z	>-	Z	z	Z	2	∢	3413
10	FLPSDFFKSV		z	>	z	z	Z	2	∢	3414
10	FLPSDFFPKV		z	>	z	z	z	2	< <	3415
	FLPSDFFPSV(CONH2)									3416
	VLEYLVSFGV(NH2)		-							3417

Table XXII	₹.			HBV	HBV ANALOGS					
A A	Sequence	Fixed Nomen.	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	1° Anchor Fixer	Analog	SEQ ID NO:
	ATVELLSFLPSDFFPSV-NH2									3418
	TVELLSFLPSDFFPSV-NH2									3419
	VELLSFLPSDFFPSV-NH2									3420
	ELLSFLPSDFFPSV-NH2									3421
	LLSFLPSDFFPSV-NH2									3422
	LSFLPSDFFPSV-NH2									3423
	SFLPSDFFPSV-NH2							•		3424
	FLPSDFFPSV-NH2									3425
	LPSDFFPSV-NH2									3426
	PSDFFPSV-NH2									3427
	FLPSDFFPS-NH2						,			3428
	FLPSDFFP-NH2									3429
	FLPSDFF-NH2									3430
	ALPSDFFPSV-NH2									3431
	SLNFLGGTTV(NH2)									3432
	FLPSDFFPSVR-NH2									3433
	ALPKDWEEL									3434
	VLGGSRHKL									3435
	KIKESFRKL									3436
	ALMPLYASI					*				3437
	FLSKOYLNL									3438
	LLGSAANWI									3439
	NLNNLNVSI									3440
	IIKKSEOFV		•							3441
	ALSLIVNLL									3442
	RIPRTPRSV									3443
										3444
										3445

Table XXIII: Immunogenicity of HBV-derived peptides

							Immunogenicity		
Supermotif	Peptide	Sequence	SEQ ID NO:	Protein	XRN	primary	transgenic	patients	overall'
A2 supermotif	924.07	FLPSDFFPSV	3492	HBV core 18	S	10/10	9/9	25/32 ^a	+
	1069.06	LLVPFVQWFV	3493	HBV env 338	5	3/4	6/9		+
	1147.13	FLLAQFTSAI	3494	HBV pol 513	~		6/0		nnk
	1090.77	YMDDVVLGV	3495	HBV pol 538	\$		6/6		+
	777.03	FLLTRILTI	3496	HBV env 183	4			14/23 ^a	+
	927.15	ALMPLYACI	3497	HBV pol 642	4	10/12	3/5	2/15 ⁸	+
	1013.01	WLSLLVPFV	3498	HBV env 335	4	7/6	6/5	23/29 ^a	+
	1069.05	LLAQFTSAI	3499	HBV pol 504	4	0/4	9/2		unk
	1132.01	LVPFVQWFV	3500	HBV env 339	4	0/3	0/4		nnk
	1147.14	VLLDYQGMLPV	3501	HBV env 259	4	4/4	9/9		+
	927.41	LLSSNLSWL	3502	HBV pol 992	က	0/4	0/3		nnk
	927.42	NLSWLSLDV	3503	HBV pol 411	٣		2/8		+
	927.46	KLHLYSHPI	3504	HBV pol 489	3	0/4	4/6		+
	1069.07	FLLAQFTSA	3505	HBV pol 503	n	1/2	0/3		+
	1168.02	GLSRYVARL	3506	HBV pol 455	3			9/13 ^a	+
A2 supermotif	927.11	FLLSLGIHL	3507	HBV pol 562	2	15/22	12/13	9/18 ₈	+
	927.47	HLYSHPIIL	3508	HBV pol 1076	. 2		10/14		+
	. 1039.03	MMWYWGPSL	3509	HBV env 360	2	3/4	0/4		+
	1069.12	YLHTLWKAGV	3510	HBV pol 147	2	2/4			+
	1137.02	LLDYQGMLPV	3511	HBV env 260	2	1/2	0/4		+
	1142.07	GLLGWSPQA	3512	HBV env 62	2	3/4	9/9		+
	1.0573	ILRGTSFVYV	3513	HBV pol 773				3/7	+
	1013.14	VLQAGFFLL	3514	HBV env 177	_	0/4	5/12		+
	1069.10	LLPIFFCLWV	3515	HBV env 378	_	3/3	0/4	275°	+
_	1069.13	PLLPIFFCL	3516	HBV env 377	-	0/4	7/12		+
	1090.06	LLVLQAGFFL	3517	HBV env 175	-	1/5	0/4		+
	1090.12	YLVSFGVWI	3518	HBV nuc 118	-	6/6			+
	1.0518	GLSPTVWLSV	3519	HBV env 338	-			3/9¢	+
	1090.14	YMDDVVLGA	3520	HBV pol 538	1	7/2	2/5	2/70	+
A3 supermotif	1147.16	HTLWKAGILYK	3521	HBV POL 149	\$	9/0	3/3	1/22	+
	1083.01	STLPETTVVRR	3522	HBV core 141	4	3/5	9/9	8/32	+
	1150.51	GSTHVSWPK	3523	HBV pol 398	4		3/6		+
	1.0219	FVLGGCRHK	3524	HBV adr "X" 1550	3	0/4			nuk
	1069.16	NVSIPWTHK	3525	HBV pol 47	က	8/0	0/3	121	+

+	+	+	+	+	+	+	+	unk	+	nnk	nnk	+
. 1/22	3/21	2722	5/28	2722	0/12	2/16	1/12	0/12		0/12		2/12
9/9	0/3	·	0/3	. 6/3								
0/4	3/6	1/4	3/8		1/3		0/4	9/2	1/4		0/4	
3	3	3	2	2	5	4	4	4	4	4	3	2
HBV pol 388	HBV pol 665	HBV pol 531	HBV pol 150	HBV adr POL 629	HBV POL 530	HBV core 19-27	HBV ENV 313	HBV POL 429	HBV X 58	HBV POL 640	HBV POL 541	HBV POL 354
3526	3527	3528	3529	3530	3531	3532	3533	3534	3535	3536	3537	3538
LVVDFSQFSR	QAFTFSPTYK	SAICSVVRR	TLWKAGILYK	KVGNFTGLY	FPHCLAFSYM	LPSDFFPSV	IPIPSSWAF	HPAAMPHLL	LPVCAFSSA	YPALMPLYA	FPHCLAFSYM	TPARVTGGVF
1069.20	1090.10	10001	1069.15	1142.05	1147.05	988.05	1145.04	1147.02	1147.06	1147.08	1145.08	1147.04
			A3 supermotif		B7 supermotif							B7 supermotif

Immunogenicity evaluation derived from primary cultures, acute patients (a-Bertoni et al, J Clin Invest 100:503, b- Rehermann et al., J. Clin. Invest 97:1655, c- Nayersina et al., J Immunol 150:4659) or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. Unk=unknown

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

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	A 11.1.					
Anugen	Allele	Cell line	Source	Sednence	SEQ ID NO:	
	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY	3539	
	A*0201	у	HBVc 18-27 F6->Y	FLPSDYFPSV	3540	
	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	3540	
	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV	3540	
	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV	3540	
	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	3540	
		GM3107	non-natural (A3CON1)	KVFPYALINK	3541	
		BVR	non-natural (A3CON1)	KVFPYALINK	3541	
A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF	3542	
	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK	3541	
A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK	3541	
A28/68	A*6801	CIR	HBVc 141-151 T7->Y	STLPETYVVRR	3543	
A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL	3544	
B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTLVYLL	3545	
B8	B*0801	Steinlin	HIVgp 586-593 Y1->F, Q5->Y	FLKDYQLL	3546	
B27	B*2705	TG2	R 60s	FRYNGLIHR	3547	
B35.	B*3501	CIR, BVR	non-natural (B35CON2)	FPFKYAAAF	3548	
B35	B*3502	TISI	non-natural (B35CON2)	FPFKYAAAF	3548	
B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF	3548	
B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY	3549	
B51		KAS116	non-natural (B35CON2)	FPFKYAAAF	3550	•
B53	B*5301	AMAI	non-natural (B35CON2)	FPFKYAAAF	3550	
B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF	3550	
Cw4	Cw*0401	CIR	non-natural (C4CON1)	QYDDAVYKL	3551	
Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	3552	
Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	3552	
۵	٠	EL4	Adenovirus E1A P7->Y	SGPSNTYPEI	3553	
К ^р		EL4	VSV NP 52-59	RGYVFQGL	3554	
ρο	•	P815	HIV-IIIB ENV G4->Y	RGPYRAFVTI	3555	
		P815	non-natural (KdCON1)	KFNPMKTYI	3556	
		P815	HBVs 28.30	יסייינועיסת יססתו	I i	

SEQ ID NO: 3567 3568 3569 3572 3566 3566 3570 3559 3571 АНААНААНААНАА АНААНААНААНАА **AHAAHAAHAAHAA** АНААНААНААНАА AHAAHAAHAAHAA YNTDGSTDYGILQINSR YLEDARRKKAIYEKKK YLEDARRKKAIYEKKK /VHFFKNIVTPRTPPY EALIHQLKINPYVLS YARFQSQTTLKQKT YPKYVKQNTLKLAT YAAFAAAKTAAAFA YARFQSQTTLKQKT YARFQSQTTLKQKT YARFQRQTTLKAAA YARFQSQTTLKQKT **OYIKANAKFIGITE PKYVKQNTLKLAT** QYIKANSKFIGITE QYIKANSKFIGITE QYIKANAKFIGITE QYIKANSKFIGITE QYIKANSKFIGITE QYIKANSKFIGITE NGQIGNDPNRDIL YKTIAFDEEARR Sequence Radiolabeled peptide ambda repressor 12-26 Lambda repressor 12-26 unknown eluted peptide Tet. tox. 830-843 S->A non-natural (ROIV) non-natural (717.01) non-natural (ROIV) non-natural (ROIV) non-natural (717.10) non-natural (717.01) non-natural (717.01) non-natural (ROIV) non-natural (760.16) 10n-natural (717.01) non-natural (ROIV Tet. tox. 830-843 MT 65kD Y3-13 Tet. tox. 830-843 HA Y307-319 MBP 88-102Y HA 307-319 HEL 46-61 Source GM3107 or L416.3 .S102.9 L257.6 **DB27.4** 1242.5 3IN 40 Sweig Herluf H0301 L255.1 CH-12 Pitout Preiss A20 .466.1 YAR KT3 MAT A20 91.7 MAT OLL LUY QA1*0301/DQB1*03(DRB1*0405 DRB1 *0802 DRB1*0803 **JRB1***1302 DRB5*0101 DRB5*0201 DRB3*0101 DRB4*0101 ORB1*1601 DRB1*0301 DRB1 *0401 DRB1*0402 DRB1*0404 DRB1 *0701 DRB1*1101 JRB1*1501 **JRB1*0901** JRB1*1201 B. Class II binding assays **DR4w15** DR4w4 DR4w14 DR51: **JR4w10** DR52 DR13 D03.1 DR12 DRS1 DR53 DR9 DR11 DR2 DR3 DR7 DR8 DR8 Mouse Species Human

Table XXV. Monoclonal antibodies used in MHC purifi

Monoclonal antibody	Specificity
W6/32	HLA-class I
B123.2	HLA-B and C
IVD12	HLA-DQ
LB3.1	HLA-DR
M1/42	H-2 class I
28-14-8S	$H-2 D^b$ and L^d
34-5-8S	H-2 D ^d
B8-24-3	H-2 K ^b
SF1-1.1.1	H-2 K ^d
Y-3	H-2 K ^b
10.3.6	H-2 IA ^k
14.4.4	$H-2 IE^d, IE^K$
MKD6	H-2 IA ^d
Y3JP	H-2 IA ^b , IA ^s , IA ^u

Table XXVI: in vitro binding of conserved HBV-derived peptides to HLA-A2-supertype alleles.

								A2-supertype	A2-supertype binding capacity (IC50 nM)	ity (IC50 nM)		. Alleles
Peptide	¥	Molecule	1st Pos	Sequence	SEQ ID NO:	Consv.	A*0201	A*0202	A*0203	A*0206	A*6802	bound 2
924.07	2	Core	81	FLPSDFFPSV	3492	95	2.5	2.1	9'9	3.0	36	S
90'6901	2	EN<	349	LLVPFVQWFV	3493	95	7.5	=	5.9	13	286	~
1147.13	9	POL	524	FLLAQFTSAI	3494	95	24	134	1.4	34	455	s
1013.0102	6	EN	346	WLSLLVPFV	3498	100	4.6	113	4.1	01	1290	4
777.03	6	ENA	183	FLLTRILTI	3496	80	8.6	<u>8</u>	1.3	61	۳,	4
927.15	6	POL	653	ALMPLYACI	3497	95	10	. 971	3.0	091	851	4
1069.05	6	POL	525	LLAQFTSAI	3499	95	20	91	3.0	1538	51	4
1132.01	6	EN	350	LVPFVQWFV	3500	95	119	287	2083	463	1	4
1147.14	=	ENA	259	VLLDYQGMLPV	3501	8	9.8	70	2.0	13	2353	4
1060177	6	POL	538 (a)	YMDDVVLGV	3495	06	5.1	8	6.7	11	1905	4
1006901	6	POL	524	FLLAQFTSA	3505	95	0.9	1654	9.1	39	870	٣
927.46	6	POL	200	KLHLYSHPI	3504	95	72	126	3.7	. 627	26667	٣
927.42	6	POL	422	NLSWLSLDV	3503	06	11	843	91	2313	404	3
1168.02	6	POL	455	GLSRYVARL	3506	.06	79	391	81	12333		C)
927.41	6	POL	418	LLSSNLSWL	3502	06	455	55	2.6	1370	4000	e
1039.031	6	ENA	360	MMWYWGPSL	3509	85	5.6	5375	833	112	3636	2
927.11	6	POL	573	FLLSLGIHL	3507	95	1.7	4300	1000	34	11429	2
1142.07	6	EN	23	GLLGWSPQA	3512	85	13	14333	286	1429		7
927.47	6	POL	203	HLYSHPIIL	3508	80	23	14333	=	2176	755	7
1137.02	0	ENA	172 ,	LLDYQGMLPV	3511	8	51		200	552	,	2
60.6901	6	ΕN	270	VLLDYQGML	3573	95	114	•	476	4111		7
1069.14	0	NUC	891	ILSTLPETTV	3574	001	238	206	130	1194	5970	2
1069.11	9	POL	147	YLHTLWKAGI	3575	<u>8</u>	313	8600	18	4000	1250	7
1142.01	6	NUC	129	LLWFHISCL	3576	8	385	21500	238	1194	4082	7
1090.12	0	NOC	147	YLVSFGVWI	3518	8	13					_
1.0518	2	EN	329	GLSPTVWLSV	3519	75	18					-
1013.1402	6	ENA	171	VLQAGFFLL	3514	95	33	2389	3704	1947	6349	-
1069.13	6	EN	388	PLLPIFFCL	3516	<u>8</u>	11		5556	3364	8511	-
01.6901	9	ENA	389	LLPIFFCLWV	3515	100	156	5375	299	2000	•	-
90:0601	9	EN	175	LLVLQAGFFL	3517	8	191	1162	2222	2467	3636	-
1.0895	9	ENA	248	FILLICLIFL	3577	80	179					-
927.24	6	POL	770	WILRGTSFV	3578	80	185					-
1090.14	6	POL	538	YMDDVVLGA	3520	8	200		4167			-
3.0205	2	ENA	171	FLGPLLVLQA	3579	75	263					-
1069.08	2	EN	760	ILLICLIFIL	3580	00	563	•		2846	26667	-
0573	9	2	773	T POT SECOND	358	S						

Frequency of entire sequence amongst isolates scanned.
 Number of superrpe alleles bound. Peptides binding 3 or more alleles are considered degenerate.
 A dash (-) indicates ICS0

Table XXVII: in vitro binding of conserved HBV-derived peptides to HLA-A3-supertype alleles.

Peptide	Ş	Molecule	1st Pos	Sequence	SEQ ID NO:	Consv.	A•03	A•11	A*3101	A*3301	A*6801	punoq
26.0535	=	X NUC FUS	299	GVWIRTPPAYR	3582	95	58	35	3.0	40	12	~
1147.16	=	lod	149	HTLWKAGILYK	3583	001	20	7	486	403	42	S
26.0539	=	POL	376	RLVVDFSQFSR	3584	95	39	5.0	7.0	24	0.1	~
26.0149	6	×	69	CALRFTSAR	3585	85	3235	761	12	3.6	=	4
1.0993	6	×	130	KVFVLGGCR	3586	75	262	73	30	408	7997	4
26.0153	6	×	64	SSAGPCALR	3587	06	1375	43	55	181	=	4
1083.01	=	Core	141	STLPETTVVRR	3588	95	733	4.0	180	181	56	4
20.0130	6	pol	655	AFTFSPTYK	3589	95	42	120	3103	13182	536	e
26.0008	œ	POL	959	FTFSPTYK	3590	95	193	136	1286	1000	7.3	٣
1.0219	6	×	1550	FVLGGCRHK	3591	8	691	316	1500	744	103	٣
1069.20	0	POL	388	LVVDFSQFSR	3592	100	6875	11	692	126	91	3
91.6901	6	POL	47	NVSIPWTHK	3593	001	134	105	۳,	2900	250	٣
1090.10	9	POL	999	OAFTFSPTYK	3594	95	244	=	18000	\$088	6.7	9
1090.11	6	POL	531	SAICSVVRR	3595	95	1897	53	1200	446	71	٣
20.0131	6	<u> </u>	524	SVVRRAFPH	3596	95	001	01	621		200	٣
26.0545	=	X NUC FUS	318	TLPETTVVRRR	3597	95	22000	375	2951	408	:	3
26.0023	8	X NUC FUS	386	VSFGVWIR	3598	06	2750	207	240	1074	222	m
1142.05	6	POL	55	KVGNFTGLY	3599	9.5	52	353			•	2
1142.06	6	7 0	623	PVNRPIDWK	3600	85	355	43	•		8889	7
1.0975	6	POL	901	RLKLIMPAR	3601	7.5	116		8.8	592	•	7
1.0562	2	7 0	576	SLGIHLNPNK	3602	7.5	55	$\iota\iota$				7
1069.21	2	NUC	170	STLPETTVVR	3603	95	15714	<u>8</u>	2250	1208	320	7
1069.22	2	NUC	171	TLPETTVVRR	3604	95	15714	761		2417	182	2
1069.15	2	POL	120	TLWKAGILYK	3605	100	2.1	11	3529	29000	615	7
1.0215	6	×	105	TTDLEAYFK	3606	7.5	18333	6.5	•	24167	471	7
1069.17	2	POL	369	VTGGVFLVDK	3607	001	282	9			3636	7
1069.19	6	POL	389	VVDFSQFSR	3608	001	7333	8	13846	1706	242	7
26.0026	∞	POL	891	ASFCGSPY	3609	100	239	92	•		20000	7
26.0549	=	ENV	389	LLPIFFCLWVY	3610	100	478	10000	5609	644	82	7
26.0550	=	POL	528	RAFPHCLAFSY	3611	95	92	15	199	26364	7997	7
1090.04	2	POL	746	GTDNSVVLSR	3612	90	11000	143	0009	15263	10000	-
1069.04	2	POL	149	HTLWKAGILY	3613	001	250	7500		8529	1999	-
1.0205	6	ZQ.	171	ILRGTSFVY	3614	80	250				•	-
1090.08	6	NUC	148	LVSFGVWIR	3615	8	3929	200				-
1039.01	2	EN	360	MMWYWGPSLY	3616	82	220	7500		•	26667	-
1.0584	2	×	104	STTDLEAYFK	3617	27	1667	2.2				-
1147.17	=	lod	735	GTDNSVVLSRK	3618	8	786	=		•	•	-
1147.18	=	lod	357	RVTGGVFLVDK	3619	100	578	202			•	-
1099.03	0	POL	120	TLWKAGILY	3620	100	85	7500			•	-
1090.15	2	POL .	549	YMDDVVLGAK	3621	8	333	1395	•	•	•	-
	•		;									

Frequency of entire sequence amongst isolates scanned.
 Number of supertpe alleles bound. Peptides binding 3 or more alleles are considered degenerate.
 A dash (-) indicates IC50

Table XXVIII: in vitro binding of conserved HBV-derived peptides to HLA-B7 supertype alleles.

												•
Peptide	¥	Molecule	1st Pos	Sequence	SEQ ID NO:	Consv.	B*0702	B*3501	B•5101	B*5301	B*5401	bound 2
1147.05	2	POL	541	FPHCLAFSYM	3623	95	S6	33	19	118	208	S
145.04	6	ENA	324	IPIPSSWAF	3624	901	42	5.6	2.3	. 21	2941	4
147.02	6	POL	440	HPAAMPHLL	3625	901	98	267	200	981	833	4
147.06	6	×	28	LPVCAFSSA	3626	95	115	101	200	10333	0.53	4
147.08	6	POL	159	YPALMPLYA	3627	95	306	150	162	664	0.63	4
988.05	6	CORE	61	LPSDFFPSV	3628	95	1774	343	9.0	120	8.4	4
1145.08	6	POL	541	FPHCLAFSY	3629	95	Μ,	4	. 88	11	503	æ
19.0014	00	POL	640	YPALMPLY	3630	061	13750	28	13	207	1786	9
26.0570	=	lod	640	YPALMPLYACI	3631	95	1375		117	291	143	m
1147.04	2	POL	365	TPARVTGGVF	3632	8	11	72		939	16667	2
15.0034	6	ENA	330	LPIFFCLWV	3633	001			57	2325	53	7
20.0140	6	POL	723	LPIHTAELL	3634	82	1375	114	1058	39	20000	7
9000'61	00	ENA	340	VPFVQWFV	3635	8	5500	•	0.29		16	7
19.0007	00	ENA	379	LPIFFCLW	3636	8		•	153	99	2857	7
0100'61	∞	POL	_	MPLSYQHF	3637	901	•	742	458	251	226	7
19.0011	∞	POL	429	HPAAMPHL	3638	001	82	18000	18	2514	625	7
19.0012	∞	POL	211	SPFLLAQF	3639	95	01	8000	306	10333	1075	7
26.0566	Ξ	<u>p</u>	511	SPFLLAQFTSA	3640	95	29				0.83	7
1147.01	٥	POL	789	DPSRGRLGL	3641	8	458		•			
16.0182	2	×	19	GPCALRFTSA	3642	8	19	٠	•		2857	-
20.0273	2	POL	440	HPAAMPHLLV	3643	82	344	3600	705	664	588	-
15.0030	6	EN	161	IPQSLDSWW	3644	8		•	27500	62		
15.0210	9	POL	123	LPLDKGIKPY	3645	<u>8</u>		248	27500		•	-
9000'91	6	EN	22	FPDHQLDPA	3646	8		8000			13	-
16.0177	2	EN	324	IPIPSSWAFA	3647	8	4231	3000		6643	22	-
16.0180	2	POL	644	APFTQCGYPA	3648	95	1897				7.1	-
16.0181	2	POL	723	LPIHTAELLA	3649	88	3056	6545		5813	30	-
19.0003	∞	EN	173	GPLLVLQA	3650	95	18333	•	200	•	1538	_
19.0005	œ	EN	313	IPIPSSWA	3651	001	13750	18000	2895		167	-
6000.61	•	NUC	133	RPPNAPIL	3652	901	724	•	196		•	-
19.0015	∞	POL	629	SPTYKAFL	3653	95	4		2895	•	•	-
9.00.61	00	POL	692	VPSALNPA	3654	8	2000		786		2	-
26.0554	=	2	633	. APFTQCGYPAL	3655	95	24	7200	13750	•	1075	-
26.0559	=	<u>z</u>	712	LPIHTAELLAA	3656	88	119	2667		277	3.6	-
1950.92	=	<u>8</u>	174	NPADDPSRGRL	3657	8	458					-
26.0564	=	Core	133	RPPNAPILSTL	3658	001	42		3056		•	-
26.0567	=	Core	49	SPHHTALRQAI	.3659	100	9.5		13750	18600		-
8950 90	=											

Frequency of entire sequence amongst isolates scanned.
 Number of superpe alleles bound. Peptides binding 3 or more alleles are considered degenerate.
 A dash (-) indicates IC50

Table XXIX: HBV derived A1- and A24-motif containing peptides

a. A1-motif peptides

		•	<u> </u>		<u> </u>	HLA-A*0101
Peptide	Molecule	Position	Sequence	SEQ ID NO:	Conserv.	binding (IC50 nM)
1069.01	Core	59	LLDTASALY	3661	75	2.1
1.0519	Core	419	DLLDTASALY	3662	75	2.3
1069.02	pol	427	SLDVSAAFY	3663	95	4.8
2.0239		1000	LSLDVSAAFY	3664	95	6.0
2.0126		1521	MSTTDLEAY	3665	7 5	29
1039.06	ENV	359	WMMWYWGPSLY	3666	. 85	78
1090.14	pol	538	YMDDVVLGA	3667	90	96
1090.09	pol	808	PTTGRTSLY	3668	85	119
1069.03	pol	124	PLDKGIKPYY	3669	100	147
1069.08	env	249	ILLLCLIFLL	3670	100	192
1069.04	pol	149	HTLWKAGILY	3671	100	381
1039.01	·	360	MMWYWGPSLY	3672	85	309
1.0774	Core	· 416	WLWGMDIDPY	3673	75	309
20.0254	pol	631	FAAPFTQCGY	3674	95	368
1.0166	pol	629	KVGNFTGLY	3675	95	368

A dash indicates IC50 nM

b. A24 -motif peptides

Peptide	Molecule	Position	Sequence	SEQ ID NO:	Conserv.	HLA-A*2402 binding (IC50 nM)
20.0271	POL	392	SWPKFAVPNL	3676	95	2.1
1069.23	POL	745	KYTSFPWLL	3677	85	2.3
2.0181	POL	492	LYSHPIILGF	3678	80	11
20.0269	ENV	236	RWMCLRRFII	3679	95	11
20.0136	ENV	334	SWLSLLVPF	3680	100	31
20.0137	ENV	197	SWWTSLNFL	3681	95	32
20.0135	ENV	236	RWMCLRRFI	3682	95	169
20.0139	POL	167	SFCGSPYSW	3683	100	169
2.0173	POL	4	SYQHFRKLLL	3684	75	182
2.0060		1224	GYPALMPLY	3685	95	245
13.0129	NUC	117	EYLVSFGVWI	3686	90	353
1090.02	core	131	AYRPPNAPI	3687	90	387
13.0073	NUC	102	WFHISCLTF	3688	80	400
20.0138	POL	51	PWTHKVGNF	3689	100	414

A dash indicates IC50 nM

overall Table XXXa: Immunogenicity of HBV-derived A2-supermotif cross-reactive peptides patients 23/29^a 9/13^a 14/23ª 2/15^a Immunogenicity transgenic 6/9 0/3 6/6 2/9 0/2 9/4 9/9 0/3 2/8 4/6 83 primary 10/12 10/10 0/4 12 0/4 4/4 0/4 0/3 XRN HBV env 338 HBV env 335 HBV env 339 HBV env 259 HBV pol 411 HBV pol 489 HBV pol 503 HBV pol 455 HBV pol.538 HBV env 183 HBV pol 642 HBV pol 504 HBV pol 992 HBV core 18 HBV pol 513 Protein SEQ ID NO: 3696 3697 3698 3699 3700 3702 3703 3704 3692 3693 3694 3695 3701 3691 VLLDYQGMLPV LVPFVQWFV YMDDVVLGV LVPFVQWFV **LLSSNLSWL** NLSWLSLDV GLSRYVARL FLPSDFFPSV FLLAQFTSAI WLSLLVPFV FLLAQFTSA ALMPLYACI LLAQFTSAI KLHLYSHPI Sequence FLLTRILTI Peptide 1168.02 1147.14 90.6901 1147.13 1090.77 1069.05 1013.01 1132.01 927.46 . 1069.07 927.15 927.42 924.07 777.03 927.41

Invest 97:1655, c- Nayersina et al., J Immunol 150:4659) or transgenic mice. A positive assessment (+) is assigned when responders have been Immunogenicity evaluation derived from primary cultures, acute patients (a-Bertoni et al, J Clin Invest 100:503, b- Rehermann et al., J. Clin. noted in one of these systems.

						Immunogenicity	genicity	
Peptide	Sequence	SEQ ID NO:	Protein	XRN	primary	transgenic	patients	overall
927.11	FLLSLGIHL	3705	HBV pol 562	2	15/22	12/13	9/15 ^a	+
927.47	HLYSHPIIL	3706	HBV pol 1076	2		10/14		+
1039.03	MMWYWGPSL	3707	HBV env 360	2	3/4	. 0/4		+
1069.12	YLHTLWKAGV	3708	HBV pol 147	2 .	2/4			+
1137.02	LLDYQGMLPV	3709	HBV env 260	2	1/2	0/4		+
1142.07	GLLGWSPQA	3710	HBV env 62	2	3/4	9/9		+
1.0573	ILRGTSFVYV	3711	HBV pol 773	-			3/7 ^b	+
1013.14	VLQAGFFLL	3712	HBV env 177		0/4	5/12		+
1069.10	LLPIFFCLWV	3713	HBV env 378	_	3/3	0/4	2/5°	+
1069.13	PLLPIFFCL	3714	HBV env 377	-	0/4	7/12		+
1090.06	LLVLQAGFFL	3715	HBV env 175	-	1/5	0/4		+
1090.12	YLVSFGVWI	3716	HBV nuc 118	-	6/6			+
1.0518	GLSPTVWLSV	3717	HBV env 338	-			3/9 ^c	+
1090.14	YMDDVVLGA	3718	HBV pol 538	-	7/2	2/5	2/7 ^b	+

Immunogenicity evaluation derived from primary cultures, acute patients (a-Bertoni et al, J Clin Invest 100:503, b- Rehermann et al., J. Clin. Invest 97:1655, c- Nayersina et al., J Immunol 150:4659) or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems.

Table XXXc: Cross-recognition of HBV pol 538 and a Lamivudine induced pol 538 variant by CTL induced with a pol 538 analog^a.

	Day 6 CTL re	Day 6 CTL response (ALU)
Stimulating peptide	HBV pol 538 (YMDDVVLGA) ^b	HBV pol 538 mutant (YVDDVVLGA)
HBV pol 538	27.8	54.2
HBV pol 538 mutant	35.3	27.9

a. CTLs were induced using the 1090.77 analog of HBV pol 538 (peptide 1090.14). 1090.77 was encoded in the DNA minigene pEP2.AOS.

b. Values shown represent the geometric mean of ALU from 2 independent cultures. Peptides loaded onto target cells were 1090.14 (HBV pol 538) or 1353.02 (a Lamivudine induced mutant of pol 538).

Tal	Table XXXIa: Imm	unogenicity	XXIa: Immunogenicity of HBV-derived A3-supermotif cross-reactive peptides	A3-sup	ermotif c	ross-reacti	ve peptid	es
						Immunogenicity	genicity	
Peptide	Sequence	SEQ ID NO:	Protein	XRN	primary	XRN primary transgenic	patients	overall 1
1147.16	HTLWKAGILYK	3719	HBV POL 149	5	9/0	3/3	1/22	+
1083.01	STLPETTVVRR	3720	HBV core 141	4	3/5	9/9	8/32	+
1150.51	GSTHVSWPK	3721	HBV pol 398	4		3/6		.+
1.0219	FVLGGCRHK	3722	HBV adr "X" 1550	3	0/4			•
1069.16	NVSIPWTHK	3723	HBV pol 47	3	8/0	0/3	1/21	+
1069.20	LVVDFSQFSR	3724	HBV pol 388	e	0/4	9/9	1/22	+
1090.10	QAFTFSPTYK	3725	HBV pol 665	3	3/6	0/3	3/21	+
1090.11	SAICSVVRR	3726	HBV pol 531	3	1/4		2/22	+

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined.

T	able XXXIb: In	nmunogenic	XXXIb: Immunogenicity of non-crossreactive HBV A3-supermotif peptides	active F	IBV A3- :	supermotif	peptides	
						Immunogenicity	genicity	
Peptide	Sequence	SEQ ID NO:	Protein	XRN	primary	XRN primary transgenic patients overall	patients	overall
1069.15	TLWKAGILYK	3727	HBV pol 150	2	3/8	0/3	5/28	+
1142.05	KVGNFTGLY	3728	HBV adr POL 629	2		0/3	2/22	+

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined.

1	Table XXXIIa:	Immunogen	e XXXIIa: Immunogenicity of HBV B7-supermotif cross-reactive peptides	superm	otif cross	s-reactive p	eptides	
						Immunogenicity	genicity	
Peptide	Sequence	SEQ ID NO:	Protein	XRN	primary	XRN primary transgenic patients overall	patients	overall
1147.05	FPHCLAFSYM	3729	HBV POL 530	5	1/3		0/12	+
988.05	LPSDFFPSV	3730	HBV core 19-27	4			2/16	+
1145.04	IPIPSSWAF	3731	HBV ENV 313	4	0/4		1/12	+
1147.02	HPAAMPHLL	3732	HBV POL 429	4	9/2		0/12	•
1147.06	LPVCAFSSA	3733	HBV X 58	4	1/4			+
1147.08	YPALMPLYA	3734	HBV POL 640	4			0/12	•
1145.08	FPHCLAFSY	3735	HBV POL 541	3	0/4			•

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined. Table XXXIIb: Immunogenicity of non-crossreactive HBV B7-supermotif peptides Immunogenicity

	s overall	+	
,	patient	2/12	
	XRN primary transgenic patients overall1		
	primary		
	XRN	2	
	Protein	HBV POL 354	
	SEQ ID NO:	3736	
	Sequence	TPARVTGGVF	
	Peptide	1147.04	

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined.

Table XXXIII. Candidate HBV-derived HTL epitopes

Selection				Conse	rvancy		-
criteria	Peptide	Mol	1st Pos	Core	Total	Sequence	SEQ ID NO
DR-supermotif	F107.01	ENV	249	100	95	ILLLCLIFLLVLLDY	3737
•	F107.02	ENV	252	95	95	LCLIFLLVLLDYQGM	3738
	1280.17	ENV	258	90	90	LVLLDYQGMLPVCPL	3739
	1186.22	ENV	332	100	100	RFSWLSLLVPFVQWF	3740
	1186.15	ENV	339	95	95	LVPFVQWFVGLSPTV	3741
	1186.06	ENV	342	95	95	FVQWFVGLSPTVWLS	3742
	1186.03	NUC	19	85	85	ASKLCLGWLWGMDID	3743
•	1186.12	NUC	24	85	85	LGWLWGMDIDPYKEF	r 3744
	857.02	NUC	50		90	PHHTALRQAILCWGELMTLA	3745
	1186.23	NUC	98	85	85	RQLLWFHISCLTFGR	3746
	27.0279	NUC	117		90	EYLVSFGVWIRTPPA	3747
	27.0280	NUC	123	95	95	GVWIRTPPAYRPPNA	3748
	1186.20	NUC	129	100	95	PPAYRPPNAPILSTL	3749
	1186.16	NUC	136	100	95	NAPILSTLPETTVVR	3750
	1186.01	POL	38	95	95	AEDLNLGNLNVSIPW	3751
	1186.17	POL	45	100	95	NLNVSIPWTHKVGNF	3752
	27.0281	POL	145	100	100	RHYLHTLWKAGILYK	3753
	1280.13	POL	406	95	95	KFAVPNLQSLTNLLS	3754
	27.0283	POL	409		85	VPNLQSLTNLLSSNL	3755
	F107.03	POL	412	90	90	LOSLTNLLSSNLSWL	3756
	1186.28	POL	416	90	90	TNLLSSNLSWLSLDV	3757
	1186.27	POL	420	100	85	SSNLSWLSLDVSAAF	3758
	F107.04	POL	523	95	95	PFLLAQFTSAICSVV	3759
	1186.10	POL	526	95	95	LAQFTSAICSVVRRA	3760
	1186.04	POL	534	95	95	CSVVRRAFPHCLAFS	3761
	F107.05	POL	538	95	95	RRAFPHCLAFSYMDD	3762
	1186.02	POL	546	90	90 .	AFSYMDDVVLGAKSV	3763
	1186.05	POL	629	85	85	DWKVCQRIVGLLGFA	3764
	1280.21	POL	637	95	95	VGLLGFAAPFTQCGY	3765
	27.0278	POL	643	75	95	AAPFTQCGYPALMPL	3766
	1186.21	POL	648	95	95	QCGYPALMPLYACIQ	3767
	1280.21	POL	694	95	95	LCQVFADATPTGWGL	3768
	27.0282	POL	750	85	85	SVVLSRKYTSFPWLL	3769
	27.0262	X	13	95	90	RDVLCLRPVGAESRG	3770
	1196 07	X	50	95 95	90	GAHLSLRGLPVCAFS	3771
	1186.07	X	60	95 95	90	VCAFSSAGPCALRFT	3772
A 1	1186.29	ENV	330	100	80	SVRFSWLSLLYPFVQ	3773
Algorithm	1280.20			85	80	RDLLDTASALYREAL	3774
	1280.19	NUC	28		55	VGNFTGLYSSTVPVF	3775
	1298.02	POL	56	90		TNFLLSLGIHLNPNK	3776
	1298.03	POL	571	95 05	75 55	YPALMPLYACIQSKQ	· 3777
	1298.05	POL	651	95 05	55		3778
	1298.06	POL	664	95 95	60	KQAFTFSPTYKAFLC	
	1280.181	POL	722	85	80	PLPIHTAELLAACFA	3779
	1280.09	POL	774	90	80	GTSFVYVPSALNPAD	3780
DR3-motif	795.05	ENV	10	•	95	PLGFFPDHQLDP	3781
•	35.0090	ENV	312	95	90	FLLVLLDYQGMLPVC	3782
	CF-03	NUC	28	85	80	RDLLDTASALYREALESPEH	3783
	35.0091	POL	18	90	65	AGPLEEELPRLADEG	3784
	35.0092	POL	34	100	85	NRRVAEDLNLGNLNV	3785
	35.0093	POL	96	85	60	VGPLTVNEKRRLKLI	3786
	35.0094	POL	120	100	100	TKYLPLDKGIKPYYP	3787
	35.0095	POL	371	100	55	GGVFLVDKNPHNTTE	3788
	35.0096	POL	385	100	45	ESRLVVDFSQFSRGN	3789
	1186.18	POL	422	95	85	NLSWLSLDVSAAFYH	3790
	35.0099	POL	666	95	55	AFTFSPTYKAFLCKQ	3791
	35.0101	X	18	95	35	LRPVGAESRGRPVSG	3792
Lower	799.01	ENV	11	80	75	PLLVLQAGFFLLTRILTIPQ	3793
conservancy	799.02	ENV	31	95		SLDSWWTSLNFLGGTTVCLG	3794
	799.04	ENV	71	95	75	GYRWMCTRRFIIFLFILLLC	3795

Table XXXIII. Candidate HBV-derived HTL epitopes

Selection			_	Conse	rvancy		
criteria	Peptide	Mol	1st Pos	Core	Total	Sequence	SEQ ID NO
	1298.01	ENV	117	80	40	PQAMQWNSTTFHQTL	3796
	1280.06	ENV	180	80	80	AGFFLLTRILTIPQS	3797
	1280.11	ENV	245	80	80	IFLFILLCLIFLLV	3798
	CF-08	NUC	120		90	VSFGVWIRTPPAYRPPNAPI	3799
	1186.25	NUC	121	95	90	SFGVWIRTPPAYRPP	3800
	1280.15	POL	501	80 .	80	LHLYSHPIILGFRKI	3801
	1298.04	POL	618	80	45	KQCFRKLPVNRPIDW	3802
•	1298.07	POL	767	80	70	AANWILRGTSFVYVP	3803
	1298.08	POL	827	80	60	PDRVHFASPLHVAWR	3804

Table XXXIV. HLA-DR screening panels

Panel Antigen Alleles Primary DR1 DRB1*0101-03 DR4 DRB1*0401-12 DRB1*0401-12 DR7 DRB1*0701-02 Panel total DRB1*1501-03 DR2 DRB5*0101 DR9 DRB1*1901-06 Panel total DRB1*1301-06 Panel total DRB1*0405 DR13 DRB1*0801-5 DR11 DRB1*0801-5 DR11 DRB1*1101-05 Panel total Panel total	Alleles DRB1*0101-03 DRB1*0401-12 DRB1*0701-02	Allele	Alias	Cauc	Blk	Jun	Cho.	Hien	•
DR 1 DR 4 DR 7 DR 2 DR 9 DR 13 Panel total DR 8 DR 11 Panel total	*0101-03 *0401-12 *0701-02							. HISP.	Avg.
DR4 DR7 Panel total DR2 DR9 DR13 Panel total DR4 DR8 DR11 Panel total	1*0401-12 1*0701-02	DRB1*0101	(DR1)	18.5	8.4	10.7	4.5	10.1	10.4
DR2 DR2 DR2 DR9 DR13 Panel total DR4 DR8 DR8 DR11	1*0701-02	DRB1*0401	(DR4w4)	23.6	6.1	40.4	21.9	29.8	24.4
Panel total DR2 DR2 DR9 DR13 Panel total DR4 DR8 DR8 DR11		DRB1*0701	(DR7)	26.2	1.1	1.0	15.0	16.6	14.0
DR2 DR9 DR13 Panel total DR4 DR8 DR11 Panel total				59.6	24.5	49.3	38.7	51.1	44.6
DR2 DR2 DR9 DR13 Panel total DR8 DR11 Panel total									
DR2 DR9 DR13 Panel total DR4 DR8 DR11 Panel total	DRB1*1501-03	DRB1*1501	(DR2w2 BI)	19.9	14.8	30.9	22.0	15.0	20.5
DR 13 Panel total DR 4 DR 8 DR 11 Panel total	ORB5*0101	DRB5*0101	(DR2w2 B2)	•			•		•
DR13 Panel total DR4 DR8 DR11 Panel total	DRB1*09011,09012	DRB1*0901	(DR9)	3.6	4.7	24.5	19.9	6.7	11.9
Panel total DR4 DR8 DR11 Panel total	DRB1*1301-06	DRB1*1302	(DR6w19)	21.7	16.5	14.6	12.2	10.5	15.1
DR4 DR8 DR11 Panel total				42.0	33.9	61.0	48.9	30.5	43.2
DR8 DR11 Panel total	B1*0405	DRB1*0405	(DR4w15)				•		-
	1*0801-5	DRB1*0802	(DR8w2)	5.5	10.9	25.0	10.7	23.3	15.1
Panel total	DRB1*1101-05	DRB1*1101	(DR5w11)	17.0	18.0	4.9	19.4	18.1	15.5
				22.0	27.8	29.2	29.0	39.0	29.4
200	0.1000#1000	1000+1000	(DD 317)	17.7	19.5	0.4	7.3	14 4	110
Quartemary DR3 DRB1	DRB1*1201-02	DRB1*1201	(DR5w12)	2.8	5.5	13.1	17.6	5.7	8.9
la .				20.2	24.4	13.5	24.2	19.7	20.4

Table XXXV. HBV-derived cross-reactive HLA-DR binding peptides

Peptide Mol						-			יייים	TLA-DA Ulliquing capacity (1000 nm	Capacity	22 1111					10 E
	1st Pos	Core	Total	Sequence	SEQ ID NO: D	DRI	DR2w2 01	DR2w2 82	DR3	DR4w4	DR4w4 DR4w15 DR5w11	DR5w11	DR6	DR7	DR8	DR9	alleles bound
•	412	8	8	LQSLTNLLSSNLSWL		2.0	21	1000	æ ,	9.4	47	294	135	167	557	682	01
1298.06 POL	66	95	3	KQAFTFSPTYKAFLC	3806	9.4	38	143		4	173	2	175	92	408	139	2
1280.06 ENV	180	8	80	AGFFLLTRILTIPQS		Ξ	217	1053	•	8.5	253	9.6	9.5	8.1	188	28	6
	774	06	80	GTSFVYVPSALNPAD		14	959	400		811	93	426		83	803	221	6
1186.25 NUC	121	95	8	SFGVWIRTPPA YRPP		532	827	47		577	603	692	17500	1042	961	938	~
27.0280 NUC	123	95	95	GVWIRTPPAYRPPNA		14	217	2.8		2	<i>L</i> 9	42		114	35	1991	00
	120		8	VSFGVWIRTPPAYRPPNAPI		192		105		300		426		124			٧.
27.0281 POL	145	<u>8</u>	8	RHYLHTLWKAGILYK		17	5.4	35	,	2250	1462	42	745	19	27	174	00
1186.15 ENV	339	95	98	LVPFVQWFVGLSPTV		385	13	1429	•	300	23	S	1944	7117	74	8	7
1280.15 POL	201	8	08	LALYSHPITLGFRKI		727	268	200	•	99	238	488	17500		803	1531	7
F107.04 POL	523	95	95	PFLLAQFTSAICSVV		28	337	4762	•	563	317	1667	4	325	845	1271	7
1298.04 POL	819	8	45	KQCFRKLPVNRPIDW		3.3	4136	952	•	38	45	1538	814	63	845	3000	7
1298.07 POL	191	8	2	AANWILRGTSFVYVP		54	379	3279		882	1520	1429	140	43	961	278	7
857.02 NUC	20		06	PHHTALRQAILCWGELMTLA		20	9.1	211		88		263	193000	929	961	2273	7

a. A dash (·) indicates IC50 nM >20,000.

Table XXXVI. HBV-derived DR3-binding peptides

			Conservancy	rvancy			
Peptide	Mol	1st Pos	Core	Total	Sequence	SEQ ID NO:	DR3
1280.14*	POL	694	95	95	LCQVFADATPTGWGL	3819	<i>L</i> 9
35.0096	POL	385	100	45	ESRLVVDFSQFSRGN	3820	115
35.0093	POL	96	85	09	VGPLTVNEKRRLKLI	3821	136
1186.27	POL	420	100	85	SSNLSWLSLDVSAAF	3822	200
1186.18	POL	422	95	85	NLSWLSLDVSAAFYH	3823	231

*tested as peptide 35.0100

Table XXXVIIa: HBV Preferred CTL Epitopes

Peptide	Sequence	SEQ ID NO:	Protein	HLA
924.07	FLPSDFFPSV	3824	core 18	A2
777.03	FLLTRILTI	3825	env 183	A2
927.15	ALMPLYACI	3826	pol 642	A2
1013.01	WLSLLVPFV	3827	env 335	A2
1090.77	YMDDVVLGV	3828	pol 538	A2/A1
1168.02	GLSRYVARL	3829	pol 455	A2
927.11	FLLSLGIHL	3830	pol 562	A2
1069.10	LLPIFFCLWV	3831	env 378	A2
1069.06	LLVPFVQWFV	3832	env 338	A2
1147.16	HTLWKAGILYK	3833	pol 149	A3/A1
1083.01	STLPETTVVRR	3834	core 141	A3
1069.16	NVSIPWTHK	3835	pol 47	A3
1069.20	LVVDFSQFSR	3836	pol 388	A3
1090.10	QAFTFSPTYK	3837	pol 665	A3
1090.11	SAICSVVRR	3838	pol 531	A3
1142.05	KVGNFTGLY	3839	pol 629	A3/A1
1147.05	FPHCLAFSYM	3840	pol 530	B7
988.05	LPSDFFPSV	3841	core 19	B7
1145.04	IPIPSSWAF	3842	env 313	B7
1147.02	HPAAMPHLL	3843	pol 429	В7
26.0570	YPALMPLYACI	3844	pol 640	В7
1147.04	TPARVTGGVF	3845	pol 354	B7
1.0519	DLLDTASALY	3846	core 419	A1
2.0239	LSLDVSAAFY	3847	pol 1000	Al
1039.06	WMMWYWGPSLY	3848	env 359	Al
20.0269	RWMCLRRFII	3849	env 236	A24
20.0136	SWLSLLVPF	3850	env 334	A24
20.0137	SWWTSLNFL	3851	env 197	A24
13.0129	EYLVSFGVWI	3852	core 117	A24
1090.02	AYRPPNAPI	3853	core 131	A24
13.0073	WFHISCLTF	3854	core 102	A24
20.0271	SWPKFAVPNL	3855	pol 392	A24
1069.23	KYTSFPWLL	3856	pol 745	-A24
2.0181	LYSHPIILGF	3857	pol 492	A24

Table XXXVIIb: HBV Preferred HTL epitopes

Selection				Conservancy	rvancy		
Criteria	Peptide	Mol	1st Pos	Core	Total	SEQ ID NO:	Sequence
DR supermotif	F107.03	POL	412	06	06	3838	LQSLTNLLSSNLSWL
	1298.06	POL	664	95	. 09	3859	KQAFTFSPTYKAFLC
	1280.06	ENA	180	80	80	3860	AGFFLLTRILTIPQS
	1280.09	POL	774	96	80	3861	GTSFVYVPSALNPAD
	CF-08	CORE	120		90	3862	VSFGVWIRTPPAYRPPNAPI
	27.0281	POL	145	100	100	3863	RHYLHTLWKAGILYK
	1186.15	ENA	339	95	95	3864	LVPFVQWFVGLSPTV
	1280.15	POL	201	80	80	3865	LHLYSHPIILGFRKI
	F107.04	POL	523	95	95	3866	PFLLAQFTSAICSVV
	1298.04	POL	618	80	45	3867	KQCFRKLPVNRPIDW
	1298.07	POL	191	80	20	3868	AANWILRGTSFVYVP
	857.02	CORE	20		06	3869	PHHTALRQAILCWGELMTLA
DR3 motif	1280.14	POL	694	95	95	3870	LCQVFADATPTGWGL
	35.0096	POL	385	100	45	3871	ESRLVVDFSQFSRGN
	35.0093	POL	96	82	09	3872	VGPLTVNEKRRLKLI
	1186.27	POL	420	100	85	3873	SSNLSWLSLDVSAAF